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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 14 Seconds

(without alignments)
1347.981 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGISTVPEDLPLPLVLELV.....DIEALCGPALPAPSLLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Swisprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2487	100.0	455	TR1A_HUMAN	P19438 homo saplen
2	1738	69.9	461	TR1A_PIG	P50555 sus scrofa
3	1563.5	62.9	461	TR1A_RAT	P22934 rattus norv
4	1521	61.2	454	TR1A_MOUSE	P25118 mus musculu
5	1517	61.0	471	TR1A_BOVIN	O19131 bos taurus
6	374	15.0	417	TR12_HUMAN	O33038 h tumor nec
7	251.5	10.1	435	TRN3_HUMAN	P36941 homo saplen
8	240.5	9.7	437	TR16_HUMAN	P08138 homo saplen
9	230	9.2	417	TR16_MOUSE	O22041 mus musculu
10	223	9.0	425	TR16_RAT	P07114 rattus norv
11	215	8.6	440	TR10B_HUMAN	O14763 homo saplen
12	212	8.5	381	TR10B_MOUSE	O9qzm4 mus musculu
13	207.5	8.3	415	TRN3_MOUSE	P02884 mus musculu
14	205.5	8.3	176	TR23_MOUSE	O9erf3 mus musculu
15	205	8.2	474	TR1B_MOUSE	P25119 mus musculu
16	201.5	8.1	180	TR22_MOUSE	O9erf2 mus musculu
17	200	8.0	326	VT2_MYXL	P29835 myxoma viru
18	196.5	7.9	416	TR16_CHICK	P18519 gallus gall
19	193	7.8	468	TR10A_HUMAN	O00220 homo saplen
20	192	7.7	325	VT2_SPYKA	P25943 homo saplen
21	191	7.7	332	TRN6_PIG	O77736 sus scrofa
22	189.5	7.6	327	TRN6_MOUSE	P25446 mus musculu
23	183.5	7.4	461	TR1B_HUMAN	P20333 homo saplen
24	179	7.2	269	TRN5_BOVIN	O28203 bos taurus
25	177	7.1	335	TRN6_HUMAN	P25445 homo saplen
26	176.5	7.1	289	TRN5_MOUSE	P27512 mus musculu
27	175.5	7.1	323	TRN6_BOVIN	P21867 bos taurus
28	174	7.0	324	TRN6_RAT	O63199 rattus norv
29	169.5	6.8	655	TR21_MOUSE	O9epus mus musculu
30	169	6.8	351	CRMB_COMPX	O73559 compox viru
31	168	6.8	401	TR1B_HUMAN	O00300 homo saplen
32	167	6.7	401	TR1B_RAT	O08727 rattus norv
33	166.5	6.7	277	TRN5_HUMAN	P25942 homo saplen

34	166.5	6.7	349	1	CRMB_CAMPS	O8uy27 camelipox vi
35	164	6.6	349	1	CRMB_VARY	P34015 varicella vir
36	161.5	6.5	297	1	XEDA_HUMAN	O9hav5 homo saplen
37	160	6.4	401	1	TR1B_MOUSE	O08712 mus musculu
38	158.5	6.4	386	1	TR10D_HUMAN	O9ubn6 homo saplen
39	158	6.4	625	1	TR11_MOUSE	O35305 mus musculu
40	157	6.3	260	1	TRN7_MOUSE	P26842 homo saplen
41	155	6.2	283	1	TR14_HUMAN	O92956 homo saplen
42	154.5	6.2	595	1	TRN8_HUMAN	P28908 homo saplen
43	149	6.0	616	1	TR11_HUMAN	O9y6g6 homo saplen
44	149	6.0	687	1	VS41_GIALA	P92127 giardia lam
45	148	6.0	1877	1	PKS_MOUSE	O04592 mus musculu

ALIGNMENTS

RESULT 1	ID	TR1A_HUMAN	STANDARD:	PRT:	455 AA.
AC	P19438;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p50)				
DE	(TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor				
DE	binding protein 1 (TBP1)].				
GN	TNFRSF1A OR TNFR1 OR TNFR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=90235285; PubMed=2158863;				
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,				
RA	Geltanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V.;				
RT	"Molecular cloning and expression of a receptor for human tumor				
RT	necrosis factor.";				
RL	Cell 61:361-370(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90235284; PubMed=2158862;				
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,				
RA	Tabuchi H., Lesslauer W.;				
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis				
RT	factor receptor.";				
RL	Cell 61:351-359(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.				
RX	MEDLINE=91006021; PubMed=1698610;				
RA	Nopar Y., Kemper O., Brekebusch C., Engelmann H., Zhang R.,				
RA	Aderka D., Holtmann H., Wallach D.;				
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA				
RT	for the type I TNF-R, cloned using amino acid sequence data of its				
RT	soluble form, encodes both the cell surface and a soluble form of the				
RT	receptor.";				
RL	EMBO J. 9:3269-3278(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91090841; PubMed=1702293;				
RA	Himmeler A., Maurer-Fogy I., Kroeck M., Scheurich P., Pfizenmaier K.,				
RA	Lantz M., Olsson I., Hauptmann R., Strotowa C., Adolf G.R.;				
RT	"Molecular cloning and expression of human and rat tumor necrosis				
RT	factor receptor chain (p50) and its soluble derivative, tumor				
RT	necrosis factor-binding protein.";				
RL	DNA Cell Biol. 9:705-715(1990).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE=Placenta;				
RC	MEDLINE=91017509; PubMed=2170974;				
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;				

Query Match 100.0%; Score 2487; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-166;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTVPDILLPLVLELLVGIYPSGYIGLVPHLGDRKSDVCPQKQYTHPONNSICTT 60
 DB 1 MGSTVPDILLPLVLELLVGIYPSGYIGLVPHLGDRKSDVCPQKQYTHPONNSICTT 60
 QY 61 KCHKGYLVNDGPGPDGDDPCRECEGSFTASENHLRHCLSCSKCRKREMGQVEISSCTVD 120
 DB 61 KCHKGYLVNDGPGPDGDDPCRECEGSFTASENHLRHCLSCSKCRKREMGQVEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFLRENECV 180
 QY 181 SCGNCKSLECTKLCPLQIENVKGTEDSGTVLLPLVIFFGCLLSLFLGLMYRYQRMK 240
 DB 181 SCGNCKSLECTKLCPLQIENVKGTEDSGTVLLPLVIFFGCLLSLFLGLMYRYQRMK 240
 QY 241 SKLYSTVCGSKTEPEKEGELGTTTKPLAPNPSFPPTGPFPTLGFSPVPSSTFTSSSTYT 300
 DB 241 SKLYSTVCGSKTEPEKEGELGTTTKPLAPNPSFPPTGPFPTLGFSPVPSSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREVPAYQCADPLATATASDPIPNPLQKWEDESAHKPQSLDTPDPTLY 360
 DB 301 PGDCPNFAAPRREVPAYQCADPLATATASDPIPNPLQKWEDESAHKPQSLDTPDPTLY 360
 QY 361 AVEENVPPLKMKFEVRLGSDHEIDRLQNGRCLEADAYSMATARRTRPREATLEL 420
 DB 361 AVEENVPPLKMKFEVRLGSDHEIDRLQNGRCLEADAYSMATARRTRPREATLEL 420
 QY 421 LGRVLRMDLLGCLLEDEIEBALCGPAALPPAPSLLR 455
 DB 421 LGRVLRMDLLGCLLEDEIEBALCGPAALPPAPSLLR 455

RESULT 2
 ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 GN (TNF-R1) (TNF-R1) (p55).
 OS TNFRSF1A OR TNFR1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Paul U.H.;
 RT Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
 RL Gene 163:263-266(1995).

- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity). - SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 DR EMBL: U1994; AAC48499.1; -.
 DR HSSP: P19438; 1TNR.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000020; TNFR_c6; 3.
 DR Pfam: PF00531; death; 1.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00017; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Receptor: Apoptosis; 21
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT FT
 FT DOMAIN 22 210
 FT TRANSMEM 211 233
 FT DOMAIN 234 461
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 195
 FT DOMAIN 340 350
 FT DOMAIN 362 447
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 194
 FT DISULFID 185 190
 FT CARBOHYD 54 54
 FT CARBOHYD 86 86
 FT CARBOHYD 145 145
 FT CARBOHYD 151 151
 SQ SEQUENCE 461 AA: 50696 MW: CD72361EC60C9D43 CRC64;

Query Match 69.9%; Score 1738; DB 1; Length 461;
 Best Local Similarity 71.6%; Pred. No. 2.3e-114;
 Matches 331; Conservative 29; Mismatches 94; Indels 8; Gaps 4;

QY 1 MGSTVPDILLPLVLELLVGIYPSGYIGLVPHLGDRKSDVCPQKQYTHPONNSICTT 60
 DB 1 MGSTVPDILLPLVLELLVGIYPSGYIGLVPHLGDRKSDVCPQKQYTHPONNSICTT 60
 QY 61 KCHKGYLVNDGPGPDGDDPCRECEGSFTASENHLRHCLSCSKCRKREMGQVEISSCTVD 120
 DB 61 KCHKGYLVNDGPGPDGDDPCRECEGSFTASENHLRHCLSCSKCRKREMGQVEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFLRENECV 180
 QY 181 SCGNCKSLECTKLCPLQIENVKGTEDSGTVLLPLVIFFGCLLSLFLGLMYRYQRMK 240

ID	TRIA	RAT	STANDARD:	PRT:	461 AA.
Db	181	SCVNCNKM-DCKNNLPLATSETRNDDQDGTGTVLLPLVIFEFGLCAFFLLVGLACFRGWMK			239
Qy	241	SKLVYGVGSKSPKREKGELEGTTPK-LAPNFSPTPEFTPLGSPVSSFTWSSSY			299
Db	240	PKLYITLICKSPKPYKEGEPEPLATPSFCPTTFSPSPSSPTTSSPVSPSSPSISPTF			299
Qy	300	TPGDCPNF--AAPRRREVAAPPYOGADPILATALASDPIMPPLQKWEDESAHK---POSTLT			353
Db	300	TPCDWSNFKVTPSPKREIAPPPOGACPIILMPMPASVPVPTPLPKWGSANSAHSAPQGLAD			359
Qy	354	DDPALLVAVENVPPPLRKMEFYRRGLSGHEDLELONGRCRLREAOYSMLATWRRTR			413
Db	360	ADPALLVAVDDVPPTPKMEFYRRGLSGHETLERLELONGRCRLREAOYSMLAEWRRTSR			419
Qy	414	REATLELLGRVLRDMDLLGCTLEDIEALCGPALPPAPSLR			455
Db	420	REATLELLGSVLRDMDLLGCTLEDIEALRGPARLAPAPHLR			461
RESULT 3					
ID	TRIA	RAT	STANDARD:	PRT:	461 AA.
AC	P22934:	Q91V30: Q91V93:			
DT	01-AUG-1991	(Rel. 19, Created)			
DT	01-MAR-1992	(Rel. 21, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)				
DE	(TNF-R1) (TNF-R1) (p55).				
GN	TNFRSF1A OR TNFR1 OR TNFR-1.				
OS	Rattus norvegicus (Rat).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91090841; PubMed=1702293;				
RA	Hummel A., Maurer-Fogy I., Kroenke M., Schenrich P., Pfizenmaier K.,				
RA	Iantzi M., Olsson I., Hauptmann R., Stratawa C., Adolf G.R.;				
RT	"Molecular cloning and expression of human and rat tumor necrosis				
RT	factor receptor chain (p60) and its soluble derivative, tumor				
RN	necrosis factor-binding protein."				
RN	DNA Cell Biol. 9:705-715(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.				
RC	STRAIN-Variants;				
RA	Furuya T., Salstrom J.L., Bina J., Hashiramoto A., Dobbins D.E.,				
RA	Wilder R.L., Remmers E.F.;				
RT	"Polymorphisms of the tumor necrosis factor receptor type 1 locus				
RT	among autoimmune susceptible and resistant inbred rat strains."				
RL	Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.				
CC	-1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric				
CC	TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits				
CC	caspase-8 to the activated receptor. The resulting death-inducing				
CC	signaling complex (DISC) performs caspase-8 proteolytic activation				
CC	which initiates the subsequent cascade of caspases (aspartate-				
CC	specific cysteine proteases) mediating apoptosis (By similarity).				
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO				
CC	HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS				
CC	PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY				
CC	WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING				
CC	PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO				
CC	TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX				
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND				
CC	NF-KAPPA B SIGNALING (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.				
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				
CC	-----				
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	CC	-----	
	DR	EMBL; M63122; AAAA2256.1; -	
	DR	EMBL; AF329976; AAK53562.1; -	
	DR	EMBL; AF329977; AAK53563.1; -	
	DR	EMBL; AF329981; AAK53567.1; -	
	DR	EMBL; AF329978; AAK53564.1; -	
	DR	EMBL; AF329979; AAK53565.1; -	
	DR	EMBL; AF329980; AAK53566.1; -	
	DR	PIR; B36353; B36353.	
	DR	HSSP; P19438; INCF.	
	DR	InterPro; IPR000488; Death.	
	DR	InterPro; IPR001368; TNFR_c6.	
	DR	Pfam; PF00020; TNFR_c6; 4.	
	DR	Pfam; PF00531; death; 1.	
	DR	ProDom; PD000771; TNFR_c6; 1.	
	DR	SMART; SM00005; DEATH; 1.	
	DR	SMART; SM0208; TNFR_3.	
	DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	
	DR	PROSITE; PS50050; TNFR_NGFR_2; 3.	
	DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	
	KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	
	FT	SIGNAL	1
	FT	CHAIN	22 461
	FT	DOMAIN	22 211
	FT	TRANSMEM	212 234
	FT	DOMAIN	235 461
	FT	REPEAT	43 82
	FT	REPEAT	83 125
	FT	REPEAT	126 166
	FT	REPEAT	167 196
	FT	DOMAIN	344 354
	FT	DOMAIN	363 448
	FT	DISULFID	44 58
	FT	DISULFID	59 72
	FT	DISULFID	62 81
	FT	DISULFID	84 99
	FT	DISULFID	102 117
	FT	DISULFID	105 125
	FT	DISULFID	127 143
	FT	DISULFID	146 158
	FT	DISULFID	149 166
	FT	DISULFID	168 179
	FT	DISULFID	182 195
	FT	DISULFID	185 191
	FT	CARBOHYD	54 54
	FT	CARBOHYD	151 151
	FT	CARBOHYD	201 201
	FT	VARIANT	230 230
	FT	VARIANT	295 295
	FT	SEQUENCE	461 AA; 50969 MW; ED23C05450FED202 CMC64;
	SQ		
		Query Match	62.9%; Score 1563.5; DB 1; Length 461;
		Best Local Similarity	64.9%; Pred. NO. 3.5e-102;
		Matches 294; Conservative 46; Mismatches 104; Indels 9; Gaps 4;	
Oy	1	MGLSTVPLDLLPIVLVELTLLGVPSGVGINVPHGIDREKRNSVCYGGKTHIPONNSICT	60
Dd	1	MCLPVLPDLISLVIALLMGLIHSGVGVLPSLDREKRNDLCQGRYAFHFKNNSICT	60
Oy	61	KCHKGTYLNDPCPGFGQDTDCRECESSGSFTYSSENILRHQLSCSKCKRMGOVEISSCTVD	120
Dd	61	KCHKGTLYVSDCPSPGGQTVCEVOCKRGFTLASQNHRQLCSCKTRKMKMPQVEIISPCKAD	120
Oy	121	RDIYCGCKRNORRYHWSENLFOCFENCSICLANGVIHALSCOEKONTYCTCHAGFFLENCY	180
Dd	121	MDIYCGCKKNOFORYLSTETHFOCYDCSPCFMGTYVIPCKERONTFCVNCHAGFFLSIGNECT	180

QY 181 SCSSCKSLSECTKCLPQIENWKTEDSGTLLPLVIFPGCLLSLFTGLMRYORWK 240
 DB 181 PCSHCKKNOCMKCLRPVANNVNPQSGAVLLVIFGLCLLFFICISLCLCRYQWR 240
 QY 241 SKLYSTYCGKSTPEKEGELGTTTKPLAPN--PSFSPTPGPTPLGSPVSSST 298
 DB 241 PRVYSITCRSDAPKVEGEGEIVTKPLTPASIFSPNPGFNPLGFTTPRSHPSST 300
 QY 299 -----YTPGDCPNFAAPRRVAPYOGADPLATATLASDPIPNPLQMED-SAHKPOSLD 352
 DB 301 PISVPEGRSMNHNVPVRVREVLP--QCADPLVGLSLNVPVPIPAVRKMEVDVAAPQRLD 359
 QY 353 TDDPATIYAVENYPRPLRMKEFVARLCLSDHEIDLRLQKCLREAOYSKLATWRKRT 412
 DB 360 TADPAMLYAVVDGVPPTRMKEFMRLLGLSEHEIERLELQNGRCLEAHYSMLLEAMRRRT 419
 QY 413 RREATLELCLVLRMDLCLGLEDIEEALCPA 445
 DB 420 RHEATLDVGRVLCMDMLRGCLNIRETLESFA 452
 RESULT 4
 TRIA_MOUSE STANDARD; PRT; 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 GN TNFRSF1A (TNF-R1) (p55).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9187885; Pubmed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9124168; Pubmed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91285014; Pubmed=1647956;
 RA Barrett K., Taylor-Fleming D.A., Cope A.P., Kissonerghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SpLien;
 RX MEDLINE=92039815; Pubmed=1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94245292; Pubmed=8188324;
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endometrialoma cell line.";

RL Immunogenetics 39:450-451(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93156721; Pubmed=8381516;
 RA Rothe J., Blüthmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175(1993).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits
 CC caspase-8 to the activated receptor. The resulting death-inducing
 CC signaling complex (DISC) performs caspase-8 proteolytic activation
 CC which initiates the subsequent cascade of caspases (aspartate-
 CC specific cysteine proteases) mediating apoptosis (by similarity).
 CC -SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -SUBCELLULAR LOCATION: Type I membrane protein.
 CC -SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M60468; AAA39751.1; -;
 DR EMBL: M59377; AAA40464.1; -;
 DR EMBL: X59238; CAA41922.1; -;
 DR EMBL: X57796; CAA40936.1; -;
 DR EMBL: L26349; AAA59361.1; -;
 DR EMBL: M7656; AAA40465.1; -;
 DR EMBL: M88067; AAA40465.1; JOINED.
 DR EMBL: M76655; AAA40465.1; JOINED.
 DR EMBL: BC004599; AAH04599.1; -;
 DR PIR: A38634; GOMSTL.
 DR PIR: S16677; S16677.
 DR PIR: S19021; S19021.
 DR HSSP: P19438; 1EXT.
 DR MGD: MGI:131484; Tnf1sfla.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR Pfam: PF00531; death; 1.
 DR PRODOM: PD000771; TNFR_c6; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT DOMAIN 22 212
 FT TRANSMEM 213 235
 FT DOMAIN 236 454
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT TNFR-CYS 4.

[illegible]

SO SEQUENCE 471 AA: 51367 MW: 5243EF514DFE81C4 CRC64;
 Query Match 61.0%; Score 1517; DB 1; Length 471;
 Best Local Similarity 62.9%; Pred. No. 6,4e-99;
 Matches 302; Conservative 38; Mismatches 104; Indels 36; Gaps 7;
 QY 1 MGLSTVDDLLPLVLELLVGIYSSVIGLVPHLGDREKSDSVPOCKYIHPQNNISICT 60
 DB 1 MGLPTVGLLLPLVPLLDVYVAGVGLPHPGDLEKRSPPCKYINPQSTICT 60
 QY 61 KCHKGTLYNDPCPGGDDTCRECESSFTASENHLRHLCSCSKREMGVETSSCTVD 120
 DB 61 KCHKGTLYNDPCPGGDDTCRECESSFTASENHLRHLCSCSKREMGVETSSCTVD 120
 QY 121 RDVYCGCRKNQYRIHYSENEFQCEKSLCLNGTVHLSCEQKONTVCTCHAGFLLRENECV 180
 DB 121 RDVYCGCRKNQYRIHYSENEFQCEKSLCLNGTVHLSCEQKONTVCTCHAGFLLRENECV 180
 QY 181 SCNSCKSLSECTKICLQIENVKCTEDSGTTLVPLVIFGICLLSLFLIGLAMYQRMK 240
 DB 181 SCHDKKKK-EECKLCPTRPSTGKSDPGTTLVPLVIFGLCLASFRASVYLACRYQRMK 239
 QY 241 SKLSYIVGKSTPEKEGELGCTTKPLAPNPSFSPGFTPTLGSPVPSSTFTSSSTYT 300
 DB 240 PKLSTIICGOSTLVKECEPE-----LVPAAGFNP-----TTTICFSSSTPSSPVSTIPIYI 290
 QY 301 PGDCPNF---AAPREVAAPYQADPIL-----ATL-----ASDP 335
 DB 291 SCDSNFGAVVSPSESTAPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCT 350
 QY 336 NPLQKWDSDA-HKPOSIDTDPAFLVAVENVPPRLKKEPRARIGLSGHEIDRLONGR 394
 DB 351 TPVQKWSASASADQDLADPAFLVAVDGPVPSRKELVRLGSEHEIERLELENGR 410
 QY 395 CLREAGYSMLATWRRTPREATELELGRVLRDMDLGLCEDEIAGLCPALPPASILT 454
 DB 411 HLRAQYSMLAAMRRTPREATELELGRVLRDMDLGLCEDEIAGLGAARLASERILL 470
 RESULT 6
 TR12_HUMAN STANDARD: PRT: 417 AA.
 ID TR12_HUMAN 093037: 092983; P78515; 099831; 099722; P78507;
 AC 099830; 098186; 014865; 014866; 000275; 000276; 000277; 000278;
 AC 000279; 000280; 090ME0; 090ME1; 090ME5;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 12 precursor
 DE (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-
 DE mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)
 DE (Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated
 DE receptor of death) (LARD).
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID:9606;
 RN 1;
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.
 RC TISSUE=Lymphoid;
 RX MEDLINE=9708617; PubMed=8934525;
 RA Kilsen J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,
 RA Glimm C.J., Brown R., Farow S.N.;
 RA "A death-domain-containing receptor that mediates apoptosis.";
 RL Nature 384:372-375(1996).
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Umbilical vein endothelial cells;
 RX MEDLINE=97081063; PubMed=8875942;
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,
 RA Duan D.R., King L., Gentz R., Ni J., Dixit V.M.;
 RA "Signal transduction by DR3, a death domain-containing receptor

RT related to TNFR-1 and CD95."; Science 274:990-992(1996).
 RN 13;
 RP SEQUENCE FROM N.A.
 RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN 14;
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Heart;
 RX MEDLINE=97148200; PubMed=8994832;
 RA Marsters S.A., Sheridan J.P., Donahue C.J., Patti R.M., Gray C.L.,
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;
 RA "Apo-3, a new member of the tumor necrosis factor receptor family,
 RA contains a death domain and activates apoptosis and NF-kappa-B.";
 RL Curr. Biol. 6:1669-1676(1996).
 RN 15;
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
 RX MEDLINE=97272273; PubMed=9114039;
 RA Screation G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
 RA Michael A.J., Bell J.I.;
 RA "LARD: a new lymphoid-specific death domain containing receptor
 RA regulated by alternative pre-mRNA splicing."; Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
 RN 16;
 RP SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
 RX MEDLINE=98113360; PubMed=9446802;
 RA Marzocha K., Ribello P., Charlot C., Renard N., Colffier B.,
 RA Salles G.;
 RA "A new death receptor 3 isoform: expression in human lymphoid cell
 RA lines and non-Hodgkin's lymphomas."; Blochem. Biophys. Res. Commun. 242:376-379(1998).
 RN 17;
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
 RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN 18;
 RP SEQUENCE OF 4-417 FROM N.A.
 RC TISSUE=Brain, and Fetal Lung;
 RX MEDLINE=97205335; PubMed=9052839;
 RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
 RA Thome M., Bornand T., Hahne M., Schroeder M., Wilson A., French L.E.,
 RA Browning J.L., MacDonald H.R., Tschopp J.;
 RA "TRAMP, a novel apoptosis-mediating receptor with sequence homology
 RA to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95)."; Immun. 6:79-88(1997).
 RN 19;
 RP SEQUENCE OF 7-417 FROM N.A.
 RC TISSUE=Brain;
 RA Chaudhary P.M., Hood L.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for TNFRSF12/APO3L/TWEAK. Interacts directly
 CC with the adaptor TRADD. Mediates activation of NF-kappaB and
 CC induces apoptosis. May play a role in regulating lymphocyte
 CC homeostasis.
 CC -1- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
 CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
 CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
 CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
 CC (potential).
 CC -1- ALTERNATIVE PRODUCTS: 12 ISOFORMS: 1/WSL-1/LARD-1A (SHOWN HERE),
 CC 2/LARD-1B, 3/WSL-3/LARD-3, 4/WSL-5/LARD-2, 5/LARD-4/LARD-11,
 CC 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND
 CC 12/BETA SOLUBLE. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
 CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
 CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
 CC -1- PTM: GLYCOSYLATED (PROBABLE).
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -1- CAUTION: Ref.5 reports for Isoform 4 at position 208 a serine

FT	VARSPLIC	54	98	MISSING (IN ISOFORM 6, ISOFORM 7 AND ISOFORM 9).
FT	VARSPLIC	54	236	MISSING (IN ISOFORM 8).
FT	VARSPLIC	156	171	SRRDTCGTCTGFEYE -> HPSVTLGORHPHSSTS (IN ISOFORM 7).
FT	VARSPLIC	172	417	MISSING (IN ISOFORM 7).
FT	VARSPLIC	182	417	MISSING (IN ISOFORM 7).
FT	VARSPLIC	182	200	MISSING (IN ISOFORM 5 AND ISOFORM 6).
FT	VARSPLIC	182	218	STLSCGRVCV (IN ISOFORM 11).
FT	VARSPLIC	182	218	STLSCGPCRCAACVGKRMQWVYLLGLVPLLLGA -> VLGGPAGPCGPPPMAGHNDLHIPILLASQAPEGCR (IN ISOFORM 3).
FT	VARSPLIC	219	417	MISSING (IN ISOFORM 3).
FT	VARSPLIC	182	277	SLSSCPBRCAACVGKRMQWVYLLGLVPLLLGATLT YTRICWPRIKPLVTADEAGMEALTPPATNLSLDSATTLA PRDSSEIKICTIVQL -> PPSLAGAPMGAAVSAPLVSVAG GRVGVGLGMRYELGELTGEGRVRGGATTOHPRAFSVLGPG APGWPCGPPMAGHNDLHIPILLASQAPEGCR (IN ISOFORM 12).
FT	VARSPLIC	278	417	MISSING (IN ISOFORM 12).
FT	VARSPLIC	200	253	MEFWOVLATGLVPLLLGATLTFTTYTHRCWPKRPVTADEAG MEALTPPATNLS -> SRMCAGNARRTGMDRGAEEGG
FT	Query Match	15.0%:	Score 374;	DB 1; Length 417;
FT	Best Local Similarity	28.3%:	Pred. No. 3.6e-19;	
FT	Matches 131;	Conservative	49;	Mismatches 183; Indels 100; Gaps 22;
QY	15 LLELLVGIYPGSVIGLVPHLDREKRSDVCCOGXKHNNPONSISCTCKHNKSTYLINDCPG	74		
Db	15 LLVLVLGARAG-----GTRSPR---COCADGFHKITGLFCRCGRGPAHYLKAPETE	63		
QY	75 PGQDTDCHECGSGSFYSSENHLR-HCLSCSKCKRMQEWVEISSCTVDIRDYVCGCKKNQYR	133		
Db	64 PCGNSTCLVCCPODPTFLAMENHNSECACQACDEASQVALENCASAVADTRCGCKPGWFV	123		
QY	134 HWMSNLRFQC-----FNCSLGIN-GTVH----LSQEKQNVTVCCHAGFFLRBNDCVSC-	182		
Db	124 EC---QVSQCVSSSFFYQPCPLDCGALKRHHRILCSNRDTCGTCPLPEFYHGOCVSCP	180		
QY	183 ----SNCKRSLECTRLCIPIENFKGTDGSGTLYLLPLVFIFGGLSLSLFIGLMYRYQR	238		
Db	181 TSTLSGCE--RCAAVC-----GWRQMHWGYLAGLVPLLLGATLTYYTRH	226		
QY	239 -WKSKLSTVCGKSTPEKEGLEGTTRYK---LAPNSFSFPFGFTPYLGFSVPVSSSTFT	294		
Db	227 CWPFR-----PLYTADAGMEALTPPATNLSPLDS-----AHLLIAPPDSEKXC	272		
QY	295 S-----SYTTTGCD-----CPNFA-----APREVAPARYGADPILATALASDPIDNPFL	338		
Db	273 TVQVLGNSEWTGYPETOBALCPQYTWSMDOLPRSRALGP-----AAPPTJSP-	318		
QY	339 QKWEDSAIRKPOSJLTDDEPATLYAVVENPPLMKFEVYRLGSDHEIDRLTLONGRCIRE	398		
Db	319 ---ESPAGSPAMIAOPGr-QLYDVMDAVPARRKMEFYRTLLDRAREIEAVAVEYIGR-FRD	373		
QY	399 AQYSMLATWRRRTPRREATLELLGRVLRDMDLCLCLEDIEBAL	441		
Db	374 QQYEMLTKRWFOQP---AGLGAVYAALERMGIDCGVEDLRSL	413		
RESULT 7				
TNR3_HUMAN	TNR3_HUMAN	STANDARD;	PRT;	435 AA.
AC	P36941;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor			
DE	(lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor).			
GN	LTR OR TNFRSF3 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Bens M., Chaffane M., Cassiman J.J., den Berghe H., Marynen P.,
 RT "Construction and evaluation of a hmdna library of human 12p
 RT transcribed sequences derived from a somatic cell hybrid."
 RL Genomics 16:214-218(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., van Arsden T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor."
 RL Science 264:707-710(1994).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells."
 RL J. Biol. Chem. 274:11868-11873(1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells."
 RL J. Biol. Chem. 275:14307-14315(2000).
 CC - FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC - SUBUNIT: Self-associates.
 CC - CELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
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 CC -----
 CC EMBL: L04270; AAA36757.1; -
 CC EMBL: BC026262; AAH26262.1; -
 CC HSSP: P25942; 1CDF.
 DR Genew; HGNC:6718; LTBFR.
 DR MIM: 600979; -
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 3.
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT TNFR-CYS 3.

FT REPEAT 169 211 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 148 BY SIMILARITY.
 FT DISULFID 142 167 BY SIMILARITY.
 FT DISULFID 170 185 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 435 AA; 46709 MW; 62462656022f656f CRC64;
 Query Match 10.1%; Score 251.5; DB 1; Length 435;
 Best Local Similarity 29.7%; Pred. No. 1,3e-10;
 Matches 106; Conservative 33; Mismatches 133; Indels 85; Gaps 22;
 Db 2 GLSTVPDLLPLVLELLVIGVPSGVIGLVPHLDREK-RDSVCPQKRYTHPONNSICQT 60
 11 GLANGP---LVGLGLGLLAASQPAV---PPYASENQCRCQD---EKEXYEPQHR-ICCS 60
 QY 61 KCHGCTLYNDCPPGQDPTDCEGSGSFTASEHRLRCLSCSKRMQGVETISSCTVD 120
 Db 61 RCPGTYVASAC-SRIRPTVCATCAENSYNEHMYLTLTQCRCQDPPVGLAEIAPCTSK 119
 QY 121 RDTVCGCRKNQRYHRYSENLEFCFNCSL---CLNGTVHLSQGE---KONTVCT-CHAGPFL 174
 Db 120 RKTGCRQCPGMCANMA---LECHTHCELLSDCPPTTELEKDEYKGNHCPCKACHF- 175
 QY 175 RENECVSCNCKSKSLCTKLCLEPQIENVKCTEDSGTT-----VL 214
 Db 176 -QNTSSPARCQPTRENOGL--VEAPGTAQSDTCKNPLEPLPMSGTMLMLAVLL 232
 QY 215 PLVTFPGCLSLFLTGLMYRQWKS-----KLYSYCKSKTPEKGELEGTGTTKPLA 268
 Db 233 PLAEFL--LTAIVFSCF-----WKSHPSLCRLKLSL--KRRQCGG----- 270
 QY 269 PNP---SFSPRPG--FTPTLGFSPV--SSTFTSSSTYVPGDQPNPAFRREAVPYQ 319
 Db 271 PNPVAGSNRPKAPHPFDVLQVPLPISGDVSPVSTGLP-----APVLEAGVPOQ 321
 RESULT 8
 TR16_HUMAN
 ID TR16_HUMAN STANDARD; PRT; 427 AA.
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 DE affinity nerve growth factor receptor) (NGF receptor) (p80-LNGBR)
 DE (p75 NTR) (Low affinity neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87051725; PubMed=3022937;
 RA Johnson D., Lashan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
 RA Bothwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor."
 RL Cell 47:545-554(1986).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=89096903; PubMed=2850481;
 RA Sehgal A., Pall N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 RL Mol. Cell. Biol. 8:3160-3167(1988).

[illegible]

```

Db      57 C-GAND-TVCCEPOLDSVFSFSDVVSATPECKPCTEC---VGLQSMSPACVBAADAVRC-- 109
Oy      130 NOYRHWSENLTQCFNCSTCLNGT-VHSCQEKONTVC-TCHAGFLRE---NECVSCS 183
Db      110 -AYGYODETTRGCCEACRCVCEAGSGVFCSCQKONTVCCECPDGTSDSEANHWDPCLPCT 168
Oy      184 NC-----KSLCEGCKLCLPPIENVKGTGEDSGTIVLPIVIFGLCLLSLFIGLMYRYORH 239
Db      169 VEDDERQRLRECTRRADACEEPIRG-----RW 195
Oy      240 KSKLIVYCGKSTPEKEGELEGGTTTKPLAPNPS---FSPTPGFTPLIGSPVPSSTFTS 296
Db      196 -----IIRSTPPESDSTAPSTOEPPEAPEDDLIASIVAGVLTIVVMSSGQVVTRGTT 248
Oy      297 STYTGDCGCFNA-----PRREVPYQAD--PIIATLADDPINPLQKNE 342
Db      249 DNLIIVYCSILAAVYVGLVYAIYAFKRWNSCKONKQANSRPVNOT-----PPEGEKLHS 303
Oy      343 DS-AHKPSLDTPDDPATLYA-----VVENPPPLR-----WKEFV 375
Db      304 DSGISVDSQSLHDQDPHTQTASGQALKGDGGLYSLLPAPKREVEKLTGNSAGDTWRHLA 363
Oy      376 RULGSDHEIDPLELQNGCGLREAOYSMATNRKRRPREATLELLGRVLRMDLIGCLE 435
Db      364 GELGQPEHID--SFTHEACPVRA--LLASW--ATQDATLDLALLALRRIO---RA 411
Oy      436 DIEEALC 442
Db      412 DLVESLC 418

RESULT 9
TR16_MOUSE
ID      TR16_MOUSE      STANDARD:      PRT:      417 AA.
AC      O92QW1:
AD      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE      affinity nerve growth factor receptor) (NGF receptor) (Low affinity
DE      neurotrophin receptor p75NTR).
GN      NGFR OR TNFRSF16
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-A:
RX      MEDLINE=96077793; PubMed=9857182;
RA      Tufturean C., Benejean J., Blondel D., Kieffer B., Flaman A.;
RT      "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RT      receptor for rabies virus."
RL      EMBO J. 17:7250-7259 (1998).
CC      -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC      AND NT-4. Can mediate cell survival as well as cell death of
CC      neural cells (By similarity). Binds to rabies virus glycoprotein
CC      Gs.
CC      -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC      associated cell death executor (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -1- PFM: N- AND O-glycosylated (By similarity).
CC      -1- PFM: Phosphorylated on serine residues (By similarity).
CC      -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC      -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC      -----
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[illegible]

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OY 363 VENVPLPKWKEFVRRLSDHIDLELQNGCRLCEADYSMTATRRRTPREATLELG 422
DB 349 -----WRHLAGELGTQPEHTID--SETHNACPVR---LLASNGAOD---SATDL 392
OY 423 RVLKRDMLGCLCEIDEALC 442
DB 393 AALRLIQ-----RADIVESLC 408

RESULT 10
TR16_RAT
ID TR16_RAT STANDARD: PRT: 425 AA.
AC P07174:
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (gp80-LINGFR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87115859; PubMed=3027580;
RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT "Gene transfer and molecular cloning of the rat nerve growth factor
RT receptor.";
RL Nature 325:593-597(1987).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93077038; PubMed=1446821;
RA Meesis M., Tammusk T., Allikmets R., Saarma M., Persson H.;
RT "Regulatory elements and transcriptional regulation by testosterone
RT and retinoic acid of the rat nerve growth factor receptor promoter.";
RL Gene 121:247-254(1992).
RN [3]
RP STRUCTURE BY NMR OF 334-418.
RX MEDLINE=97449145; PubMed=9305641;
RA Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL EMDb J.15:4939-5005(1997).
CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
CC and NT-4. Can mediate cell survival as well as cell death of
CC neural cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
CC associated cell death executor.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- AND O-glycosylated.
CC -1- PTM: Phosphorylated on serine residues.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, X05137; CA28783.1; -
DR EMBL, X61269; -; NOT_ANNOTATED_CDS.
DR PIR, A26431; A26431.
DR PDB, INGR: 29-JUL-97.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 4.
DR Pfam: PF00531; death; 1.

```

Query Match	9.0%	Score 223	DB 1	Length 425
Best Local Similarity	23.2%	Pred. No. 1.3e-08		
Matches 115	Conservative 50	Mismatches 170	Indels 160	Gaps
DR SMART; SMO0005; DEATH; 1.				
DR PROSITE; PS00652; TNFR_NGFR_1; 3.				
DR PROSITE; PS50050; TNFR_NGFR_2; 4.				
DR PROSITE; PS50017; DEATH_DOMAIN; 1.				
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;				
RV Repeat; Phosphorylation; Signal; 3D-structure.				
FT SIGNAL	1	29		
FT CHAIN	30	425	TUMOR NECROSIS FACTOR RECEPTOR	
FT			SUPERFAMILY MEMBER 16.	
FT TRANSMEM	30	251	EXTRACELLULAR (POTENTIAL).	
FT DOMAIN	252	273	POTENTIAL.	
FT REPEAT	274	425	CYTOPLASMIC (POTENTIAL).	
FT REPEAT	32	65	TNFR-CYS 1.	
FT REPEAT	67	108	TNFR-CYS 2.	
FT REPEAT	109	147	TNFR-CYS 3.	
FT REPEAT	149	189	TNFR-CYS 4.	
FT DOMAIN	354	419	DEATH.	
FT DOMAIN	198	249	SER/THR-RICH.	
FT DISULFID	33	44	BY SIMILARITY.	
FT DISULFID	45	58	BY SIMILARITY.	
FT DISULFID	48	65	BY SIMILARITY.	
FT DISULFID	87	84	BY SIMILARITY.	
FT DISULFID	100	108	BY SIMILARITY.	
FT DISULFID	90	108	BY SIMILARITY.	
FT DISULFID	110	123	BY SIMILARITY.	
FT DISULFID	126	139	BY SIMILARITY.	
FT DISULFID	129	147	BY SIMILARITY.	
FT DISULFID	150	165	BY SIMILARITY.	
FT DISULFID	168	181	BY SIMILARITY.	
FT DISULFID	171	189	BY SIMILARITY.	
FT CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	71	71	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO SEQUENCE	425 AA;	45432 MW;	B2E152D94D3827F8	CRC64;
Query Match	9.0%	Score 223	DB 1	Length 425
Best Local Similarity	23.2%	Pred. No. 1.3e-08		
Matches 115	Conservative 50	Mismatches 170	Indels 160	Gaps
DR SMART; SMO0005; DEATH; 1.				
DR PROSITE; PS00652; TNFR_NGFR_1; 3.				
DR PROSITE; PS50050; TNFR_NGFR_2; 4.				
DR PROSITE; PS50017; DEATH_DOMAIN; 1.				
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;				
RV Repeat; Phosphorylation; Signal; 3D-structure.				
FT SIGNAL	1	29		
FT CHAIN	30	425	TUMOR NECROSIS FACTOR RECEPTOR	
FT			SUPERFAMILY MEMBER 16.	
FT TRANSMEM	30	251	EXTRACELLULAR (POTENTIAL).	
FT DOMAIN	252	273	POTENTIAL.	
FT REPEAT	274	425	CYTOPLASMIC (POTENTIAL).	
FT REPEAT	32	65	TNFR-CYS 1.	
FT REPEAT	67	108	TNFR-CYS 2.	
FT REPEAT	109	147	TNFR-CYS 3.	
FT REPEAT	149	189	TNFR-CYS 4.	
FT DOMAIN	354	419	DEATH.	
FT DOMAIN	198	249	SER/THR-RICH.	
FT DISULFID	33	44	BY SIMILARITY.	
FT DISULFID	45	58	BY SIMILARITY.	
FT DISULFID	48	65	BY SIMILARITY.	
FT DISULFID	87	84	BY SIMILARITY.	
FT DISULFID	100	108	BY SIMILARITY.	
FT DISULFID	90	108	BY SIMILARITY.	
FT DISULFID	110	123	BY SIMILARITY.	
FT DISULFID	126	139	BY SIMILARITY.	
FT DISULFID	129	147	BY SIMILARITY.	
FT DISULFID	150	165	BY SIMILARITY.	
FT DISULFID	168	181	BY SIMILARITY.	
FT DISULFID	171	189	BY SIMILARITY.	
FT CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT CARBOHYD	71	71	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SO SEQUENCE	425 AA;	45432 MW;	B2E152D94D3827F8	CRC64;

Db 406 IQ----RADYESLIC 416

RESULT 11

ID	T10B_HUMAN	STANDARD:	PRT:	440 AA.
AC	014763	015531; 015508; 015517; 014720; Q9BE0;		
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2).			
DE	TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[11]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.			
RC	TISSUE=ForeSkln fibroblast;			
RX	MEDLINE=97459925; PubMed=9311998;			
RA	Malczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Naugh J.Y., Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.,			
RA	"TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL."			
RL	EMBO J. 16:5386-5397(1997).			
RN	[12]			
RP	SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE SPLICING.			
RC	MEDLINE=97431692; PubMed=9285725;			
RX	Scirelon G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.;			
RA	"TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL."			
RL	Curr. Biol. 7:693-696(1997).			
RN	[13]			
RP	SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.			
RC	TISSUE=Liver, and Spleen;			
RX	MEDLINE=98039016; PubMed=9373179;			
RA	Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschopp J.;			
RA	"Characterization of two receptors for TRAIL."			
RL	FEBS Lett. 416:329-334(1997).			
RN	[14]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	TISSUE=Ovary;			
RX	MEDLINE=97467719; PubMed=93265928;			
RA	Wu G.-S., Burns T.F., McDonald E.R. III, Jiang W., Meng R., Springer I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., KILIER/DR5 is a DNA damage-inducible p53-regulated death receptor gene."			
RL	Nat. Genet. 17:141-143(1997).			
RN	[15]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;			
RX	"An antagonist decoy receptor and a death domain-containing receptor for TRAIL."			
RL	Science 277:815-818(1997).			
RN	[16]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RC	MEDLINE=97467318; PubMed=9325248;			
RA	MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;			
RA	"Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL."			
RL	J. Biol. Chem. 272:25417-25420(1997).			
RN	[17]			
RP	SEQUENCE FROM N.A. (SHORT ISOFORM).			
RX	MEDLINE=98090092; PubMed=9433027;			
RA	Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;			


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Db 128 PCTTRNRYVOCCEGTFRDEDSPEM--CRKRTGCPRGAVKYGDCOTPMWDICVHKESE- 184
Oy 166 CTHAGFLRENEVCSCSNCKSLCTKLCLPOIENVKGTEDSGTTLVPLVIFGICLL 225
Db 185 -TKHSGEAPAVEIETSSGTPASPC-----SLSGIIIGVVAAYLVAVFVC-K 233
Oy 226 SLLEFGIMTRVORMSKSLYST--VC--GKSTPEKEGELGTTTKPLAPNPSFSP-----T 276
Db 234 SL-----WKVLPYKLGICSGGGGDPDR--VDRSSORGAEDNVLNEIYSILO 280
Oy 277 PGFTPLGSPVPSSTFTSSSTYTPGDCPNFAAP-----RRGAPPYOGADPILATA 328
Db 281 PVOVEBOEMEVEPAPDPGCVNMLSPGSEHLEPPAERSQRRLIVPANEG----- 332
Oy 339 LASDIPNPLQKEDSAHKPOSILDDPATLYAVENVPPLKWEKFEVRRLGSDHEIDL 388
Db 333 ---DPTETLRQCFDDFA-----DLVPFDSMEPLKRLGLMDNEI-KV 370
Oy 369 ELQNGRCLEAOYSMLATWRRRTPRREATLELGRVLRMDLGLCLEDIEEAL 441
Db 371 AKAEAGHRDLYTMLIKWVNKT-----GRDASVHTLLDALLETIGERTL 413

RESULT 12
ID T10B_MOUSE STANDARD: PRT: 381 AA.
T10B_MOUSE
AC 09QZM4; 09JUL5; 09JUL6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death
DE receptor 5) (Mk).
GN TNFRSF10B OR DR5 OR KILLER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99310501; PubMed=10383128;
RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of
RT the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand
RT (TRAIL) death receptor."
RL Cancer Res. 59:2770-2775(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFRSF10/TRAIL. The
CC adaptor molecule FADD recruits caspase-8 to the activated
CC receptor. The resulting death-inducing signaling complex (DISC)
CC subsequent cascade of caspases (aspartate-specific cysteine
CC proteases) mediating apoptosis. Promotes the activation of NF-
CC kappaB.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By
CC similarity)
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL: AF176833; AAD52656.1; -
CC EMBL: AB031081; BAA96462.1; -
CC EMBL: AB031082; BAA96463.1; -
CC HSSP: O14763; IDOG.
CC MGD: MGI:1341090; Tnftrsf10b.
CC InterPro: IPR000488; Death.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 2.
CC SMART: SM00005; DEATH; 1.
CC SMART: SM00208; TNFR; 2.
CC PROSITE: PS50017; DEATH_DOMAIN; 1.
CC PROSITE: PS00652; TNFR_NGFR_1; FALSE_NEG.
CC PROSITE: PS00500; TNFR_NGFR_2; 2.
CC KEGG: Receptor; Apoptosis; Transmembrane; Repeat; Signal.
CC SIGNAL 1 52
CC CHAIN 53 381
CC FT DOMAIN 53 160
CC FT TRANSMEM 161 181
CC FT DOMAIN 182 381
CC FT REPEAT 26 86
CC FT REPEAT 87 129
CC FT REPEAT 130 169
CC FT DOMAIN 273 356
CC FT DISULFID 74 85
CC FT DISULFID 88 105
CC FT DISULFID 108 121
CC FT DISULFID 111 129
CC FT DISULFID 131 145
CC FT DISULFID 148 161
CC FT DISULFID 151 169
CC FT CONFLICT 42 169
CC FT CONFLICT 97 97
CC FT CONFLICT 128 128
CC FT CONFLICT 180 180
CC FT CONFLICT 187 187
CC FT CONFLICT 215 215
CC FT CONFLICT 229 229
CC FT CONFLICT 306 306
CC SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 8.5%; Score 212; DB 1; Length 381;
Best Local Similarity 21.6%; Pred. No. 6.6e-08;
Matches 85; Conservative 44; Mismatches 127; Indels 138; Gaps 14;

Oy 62 CHKRTLYNDGCPGODDIDRCESG-SFTASENH-LRHCLSCSKCKRMGOYEISCTV 119
Db 74 CIAGQYL-----SEGNCKPCRGIDYVTSNHSNLSLSCILCTVCKEDK----- 115
Oy 120 DDDYCGGCKKNQRYHWYSENLFQGCNSCLNGTAYHLSQEQKQNVCTCHGFEFLRENE- 178
Db 116 -----VETRCNITTTNVCCKCKPTEFDKOSP 142
Oy 179 --CVSCSNCKSLCTKLCLPOIENVKGTEDSGTTLVPLVIFGICLSLFTG--LMY 234
Db 143 EICQSCSNCKTDEEELTSCPTR-ENRKCVSKTAMSMHKLGLMIGLIVPVYLLIALLVM 201
Oy 235 KQKWKSKSLIVCGKSPKEKEGELGTTTKPLAPNPSFSP-----PGFTPLGFS 286
Db 202 KIGAWROWL--LCIKRCGERDPESANSVHLSLDROHSTFTNDSNHNTEPKTQGTG-- 256
Oy 281 PVPSTFTSSSTYTPGDCPNFAAPRRREVAAPPYOGADPILATLADPILPNLQKEDSAH 346
Db 237 -----KKLLVPVNGND----- 267
Oy 347 KPOSIDTDDPATLYAVENVPPL-RWKEFEVRRLGSDHEIDLLEQNGRCLEAOYSMLA 405
Db 268 -----SADDLKRITFEYCSIDYVFPDSMNRLMRQGLGTLDNQIGWAKET-LVTRREALYOMLL 321

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OY 406 TWRRTPREATTELLGRLVRLMDLGLCEIDEE 439
 DB 322 KWRHOT-----GHSASINHLDLALFAVER 345

RESULT 13
 TNR3_MOUSE STANDARD: PRT: 415 AA.

AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTRR OR TNFRSF3 OR TNFR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression".
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 sequence trap and chromosomal mapping".
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 and TRAF6. May play a role in the development of lymphoid organs
 (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -----
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CC -----
 DR EMBL: U29173; AAA68964.1; -;
 DR EMBL: L38423; AB008446.1; -;
 DR EMBL: U30798; AA81334.1; -;
 DR HSSP: O14763; ID0G.
 DR MGD: MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR PRODOM: PD000771; TNFR_C6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT POTENTIAL.
 FT TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPRAFAMILY MEMBER 3.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 223
 FT DOMAIN 224 244
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81
 FT TNFR-CYS 1.
 FT REPEAT 82 124
 FT TNFR-CYS 2.
 FT REPEAT 125 170
 FT TNFR-CYS 3.

FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 142 150 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 BY SIMILARITY.
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 8.3%; Score 207.5; DB 1; Length 415;
 Best Local Similarity 26.8%; Pred. No. 1.5e-07;
 Matches 96; Conservative 37; Mismatches 158; Indels 67; Gaps 17;

OY 2 GLSTVPDLLPLVLELLVGPVIGLVPHLGRDRSDVCPGKYIHPONNISCTK 61
 DB 11 GLAMP---LILGLSLGLVASQPQ---LVPPY--RIENQTCMDQDKRYEPMHVDCCSR 61

OY 62 CHKGILYNDPGRQDPTDCRECESGFTASENHRHLSCKSKCKEKGVEISSCTYDR 121
 DB 62 CPGEFVFAVC--SRQDVTCTCPHNSYNEHMHLSQCLRPDCIVIGFEVAPCTSDR 120

OY 122 DTVCGCRKQYRHWSEMLFOCFNCS---LCUNGTHLSQEKQNT---VCTCHAGPF 173
 DB 121 KAECHCQPGMAGCYILDN---ECVHCEERLYLCOGFTAEVTDIMTDVNCVPCPKGHF 177

OY 174 LRENECVSCNCKKSLCTKLCLOPIENVKGTEDSGT-----TVLLPLVIF 219
 DB 178 --QNTSPRARCQPHTRCEIQL--VEAPAGSVSDTICKNPPERGAMLLAILLSLVLF 233

OY 220 FGLCLSLFLFGLM---YRQRMKSKLYSYVCKSGSTPEKEGELGTTTKPLAPPSRP 275
 DB 234 -----LLEFTVYLACAMRHPSLCKRLGTLT--KRHEGE-----ESPCCPAPRADP 277

OY 276 TPGFPTPLGFPVPSFTSSSTVTPGDCPNPAARRVAPPGACDPLITATLASDP 333
 DB 278 ---HPDLAEPPLPMSGLSPS---PAGPP--TAFSEEVYVLOOQSPVQARELEAEP 327

RESULT 14
 TR23_MOUSE STANDARD: PRT: 176 AA.

AC Q9ER63; Q8VHC0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis
 factor receptor p60 homolog 1) (TNF receptor family member SOB).
 GN TNFRSF23 OR TNFRSF11L OR TNFRH1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Embryonic stem cells;
 RX MEDLINE=20519229; PubMed=11063728;
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
 RA Lane N., Reik W., Walter J.;
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region:
 implications for a novel imprinting centre and extended imprinting.";
 RT Hum. Mol. Genet. 9:2691-2706(2000).
 RL [2]
 RP SEQUENCE FROM N.A.
 RP Pan G., Mao W., Rissler P.;
 RA "Characterization of SOB, a member of the TNFR family.";
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL)
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL)
SO	SEQUENCE	474 AA;	50319 MM;	462AE398C4D6563 CRC64;

SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match	8.28;	Score 205;	DB 1;	Length 474;
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Best Local Similarity 26.4%; Pred. No. 2.6e-07;
Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11.

Best Local Similarity 26.4%; Pred. No. 2.6e-07;
Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11.

```

OY 44 CPOGKUYTHPUNNSJCCRCRKHNGTYLYNDGPGODTDCRECESSGFYASENHLRHCLSC - 102
Db 40 CQISEGYEYDRKAQMCCKACPPGQYVKNHFC - NKTSDTYCACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCRKEMGOVEISCTYDRDTVGCGRKNQY --- RHYWSENLFQCFNCSJCLNG - TYHLS 157
Db 99 SSCFTD - QVEIRCTCKONRVCAACEGRYCALKTH - SSSCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC - CHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK - TEDSGTVLL 214
Db 155 RAPGNVLTCKKCACTGF - SFTTSSTDVCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGIMRYRQWMSKXLSYVCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV ----- SQPEP ----- TRSQPLDQEBGPS 236
OY 275 PTPGPTPIHGSFV 288
Db 237 QTPSILTSVSGSTPI 250

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OY  44  CPOGKUYTHPUNNSJCCRCRKHNGTYLYNDGPGODTDCRECESSGFYASENHLRHCLSC - 102
Db   40  CQISEGYEYDRKAQMCCKACPPGQYVKNHFC-NKTSDTYCACCEASMYQVWNOGRTCLSCS  98
OY  103  SKCKREMGQVEISCTYDRODTVGCGRKNQY---RHYWSENLFQCFNCSJCLNG-IYHLS  157
Db   99  SSCFTD--QVEIRCTCKONRVCAACEGRYCALKTH--SSGCRQCMRLSKCGPFGVASS  154
OY  158  CQEKONTVC-VCHAGFLRENECVSCSNCKSLECTKICLPQIEBNVGK--TEDGGTVLL  214
Db   155  RAPGNVULCKKCAAGTF--SITTSSTDYCRHRICSLTALPAGNASTAVCAPEPITLSAI  212
OY  215  PLVTFEGICLLSLFLGILMYRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS  274
Db   213  PRTLYV-----SQPEP-----TRSQPLDQEBGPS  236
OY  275  PTPGPTPIHGSFV  288
Db   237  QTPSILTSVLSGTPI  250

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OY 44 CPOGKYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESSGFYASENHLRHJLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAKCPFGQYVHKFC - NKTSDTYACACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREKGOVEISCTYDRDTVGCGRNQY --- RHVSENLEFCFNCISJCLNG - IYHLS 157
Db 99 SSCFTD - QVEIRCTCKONRVCAACEGRYCALKTH - SSSCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC - CHAGFLRENECVSCSNCKSLECTKICLPOIEBVGK - TEDGGTVLL 214
Db 155 RAPGNVLTCKKCACTGF - SFTTSSTDVCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGIMRYRQWMSKXLSYVCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV ----- SQPEP ----- TRSQPLDQEBGPS 236
OY 275 PTPGPTPIHGSFV 288
Db 237 QTPSILTSVSGSTPI 250

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OY 44 CPOGKUYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESGFFVASENHJHCLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAPRPGQYVKNHC- NKTSDTYCACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVGCGRNQY----RHYWSENLFQCFNCSJCLNG-IYHLS 157
Db 99 SSCFTD--QVEIRCTCKONRVCAACEGRYCALKTH--SSGCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC-VCHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK--TEDGGTVLL 214
Db 155 RAPGNVLTCKKCAAGTF--SSTTSSTDYCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGILMYRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV-----SQPEP-----TRSQPLDQEBGPS 236
OY 275 PTPGPTPIHGSFV 288
Db 237 QTPSILTSVSGSTPI 250

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OY  44  CPOGKUYTHPUNNSJCCRCRKHNGTYLYNDGPGODTDCRECESSGFYASENHLRHCLSC - 102
Db   40  CQISEGYEYDRKAQMCCKACPPGQYVKNHFC-NKTSDTYCACCEASMYQVWNOGRTCLSCS 98
OY  103  SKCKREKGOVEISCTYDRODTVGCGRKNQY---RHYWSENLFQCFNCSJCLNG-IYHLS 157
Db   99  SSCFTD--QVEIRCTCKONRVCAACEGRYCALKTH--SSGCRQCMRLSKCGPGFVASS 154
OY  158  CQEKONTVC-VCHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK--TEDSGTVLL 214
Db   155  RAPGNVLTCKKCAAGTF--SITTSSTDYCRHRICSLTALPGANSTAYVCAPEPITLSAI 212
OY  215  PLVTFGICLLSLFLGILMYRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db   213  PRTLYV-----SQPEP-----TRSQPLDQEBGPS 236
OY  275  PTPGPTPIHGSFV 288
Db   237  QTPSLTSLVSGSTPI 250

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OY 44 CPOGKUYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESGFFVASENHJHCLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAPRPGQYVKNHC- NKTSDTYCACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVGCGRNQY----RHYWSENLFQCFNCSJCLNG-IYHLS 157
Db 99 SSCFTD--QVEIRCTCKONRVCAACEGRYCALKTH--SSGCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC-VCHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK--TEDGGTVLL 214
Db 155 RAPGNVLTCKKCAAGTF--SSTTSSTDYCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGILMYRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV-----SQPEP-----TRSQPLDQEBGPS 236
OY 275 PTPGPTPIHGSFV 288
Db 237 QTPSILTSVSGSTPI 250

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OY 44 CPOGKUYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESGFFVASENHJHCLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAPRPGQYVKNHC- NKTSDTYCACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVGCGRNQY----RHYWSENLFQCFNCSJCLNG-IYHLS 157
Db 99 SSCFTD--QVEIRCTCKONRVCAACEGRYCALKTH--SSGCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC-VCHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK--TEDGGTVLL 214
Db 155 RAPGNVLTCKKCAAGTF--SSTTSSTDYCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGILMYRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV-----SQPEP-----TRSQPLDQEBGPS 236
OY 275 PTPGPTPIHGSFV 288
Db 237 QTPSILTSVSGSTPI 250

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OY 44 CPOGKYTHPNNNSJCCPKCHHGTLYLNDGPGODTDCRECESGFYASENHJHCLSC - 102
Db 40 CQISEGYEDRAQMGCAKCPFGQYVHKFC - NKTSDYCACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVGCGRNQY --- RHYWSENLFQCFNCSJCLNG - IYHLS 157
Db 99 SSCFTD - QVEIRCTCKONRVCAACEGRYCALKTH - SSSCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC - CHAGFLRENECVSCSNCKSLECTKICLPJQIEBVGK - TEDGGTVLL 214
Db 155 RAPGNVLTCKACAGTF - SPTTSTDYCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGIMRYQWMSKXLSYVCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV ----- SQPEP ----- TRSQPLQJEBPS 236
OY 275 PTFGPPTLGRSPV 288
Db 237 QTPSLTSLGSGTPI 250

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```

OY 44 CPOGKUYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESSGFYASENHLRHJLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAKCPFGQYVHKFC - NKTSDTYACACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVCCGRKNQY --- RHVSENLEFCFNCISJCLNG - IYHLS 157
Db 99 SSCFTD - QVEIRCTCKONRVCAACEGRYCALKTH - SSSCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC - CHAGFLRENECVSCSNCKSECTKICLCPQIEBVGK - TEDGGTVLL 214
Db 155 RAPGNVLTCKKCACTGF - SPTTSTSDVCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGIMRYQOMWSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV ----- SQPEP ----- TRSQPLDQEBPS 236
OY 275 PTFGPPTLIGFSpy 288
Db 237 QTPSLTSLSGSTPI 250

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OY 44 CPOGKUYTHPONNNSJCCPKCHHGTLYLNDGPGODTDCRECESSGFYASENHLRHJLSC - 102
Db 40 CQISEGYEYDRKAQMCCKAKCPFGQYVHKFC - NKTSDTYACACCEASMYQVWNOGRTCLSCS 98
OY 103 SKCKREMGQVEISCTYDRDTVCCGRKNQY --- RHVSENLEFCFNCISJCLNG - IYHLS 157
Db 99 SSCFTD - QVEIRCTCKONRVCAACEGRYCALKTH - SSSCRQCMRLSKCGPFGVASS 154
OY 158 CQEKONTVC - CHAGFLRENECVSCSNCKSLECTKICLPJOIEBVGK - TEDSGTVLL 214
Db 155 RAPGNVLTCKKCAQGT - SFTTSSTDVCRHRICSLTALPGANSTAVCAPEPITLSAI 212
OY 215 PLVTFGICLLSLFLGIMRYQWMSKXLSIYCGKSTPEKEGLEGTTRKPLAPNDFS 274
Db 213 PRTLYV ----- SQEP ----- TRSQPLQDEBPS 236
OY 275 PTPGPTPIIGFSpy 288
Db 237 QTPSILTSLSGSTPI 250

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Search completed: December 27, 2002, 15:08:38
Job time : 15 secs

Job time : 15 secs

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PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 PT and -beta, useful as therapeutic agent.
 XX
 PS Disclosure; Fig 21: 142pp; English.
 CC The sequence comprises the entire 30 kD TNF inhibitor. The clone
 CC from which the sequence was deduced was isolated from a cDNA
 CC library prep'd. from RNA form 1937 cells treated with PMA/PMA.
 CC The whole gene can be inserted into expression vectors for prep'n.
 CC of TNF inhibitor for use in the treatment of inflammatory and
 CC degenerative diseases. The active protein is claimed (Claim 8).
 CC See also AAR10984 and AAR11001.
 CC
 XX

Sequence 455 AA:

Query Match 100.0%; Score 2487; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLPHLDREKRDVCPQGYTHPONNSICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLPHLDREKRDVCPQGYTHPONNSICT 60
 QY 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 DB 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 QY 121 RDTVCGCRKNQRYHWSENLFCFCNCSICLNGTVHLSQCEKONTVCTCHAGFLENECV 180
 DB 121 RDTVCGCRKNQRYHWSENLFCFCNCSICLNGTVHLSQCEKONTVCTCHAGFLENECV 180
 QY 181 SCSNCKKSECTKCLLPQIENKVGTEDSGTVLLPLVIFGCLSLFLGLMYRYORMK 240
 DB 181 SCSNCKKSECTKCLLPQIENKVGTEDSGTVLLPLVIFGCLSLFLGLMYRYORMK 240
 QY 241 SKLYSIVCGKSTPEKEGEGTTRKPLADNPSFSPPTGFTPLIGSPVSSFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGEGTTRKPLADNPSFSPPTGFTPLIGSPVSSFTSSSTYT 300
 QY 301 PDDCNFAPRREVAPRYOGADPILATASDPINPDLQKWDSDAHKPOSJLTDPAATLY 360
 DB 301 PDDCNFAPRREVAPRYOGADPILATASDPINPDLQKWDSDAHKPOSJLTDPAATLY 360
 QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLDELONGRCLEAQSMLATWRRTTREATTEL 420
 DB 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLDELONGRCLEAQSMLATWRRTTREATTEL 420
 QY 421 IGRVLRMDLGLCLDIEALCGPALPPAPSLR 455
 DB 421 IGRVLRMDLGLCLDIEALCGPALPPAPSLR 455

RESULT 2

ID AAR42059 standard; Protein: 455 AA.

AC AAR42059;

XX 29-APR-1994 (first entry)

DE Lambda derived TNF-R.

XX Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
 KW IL-1R; fusion protein; linker: TNF; IL-1; cachexia; cerebral malaria;
 KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
 KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
 KW graft versus host disease; sepsis; inflammation; allergy;
 KW autoimmune dysfunction.

OS Homo sapiens
 XX Lambda-glt0-7ctnfbp.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..40
 FT /note= "Signal peptide"
 FT Protein 41..455
 FT /note= "Mature hTNF-R"

XX MOJ319777-A.

XX 14-OCT-1993.

XX 26-MAR-1993; 93WO-US02938.

XX 30-MAR-1992; 92US-0860710.

XX (IMM) IMMUNEX CORP.

XX Smith CA;

XX WPI: 1993-336592/42.

XX N-PSDB: AAQ49932.

PT New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.

PS Disclosure; Page 57-59; 85pp; English.

CC The sequences given in AAR42058-59 represent human tumour necrosis
 CC factor receptor (TNF-R) and the sequences in AAR42060-61 represent
 CC human interleukin-1 receptor (IL-1R). These sequences were used in
 CC the production of a fusion protein which conformed to one of the
 CC formulae:

CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R

CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 CC Ser, Thr and Ala. These linkers separate the individual moieties
 CC by such a distance that each component of the fusion protein is
 CC capable of folding into the secondary or tertiary structure required
 CC for its biological activity. These fusion proteins may be used in
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft versus
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.

XX Sequence 455 AA:

Query Match 100.0%; Score 2487; DB 14; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLPHLDREKRDVCPQGYTHPONNSICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLPHLDREKRDVCPQGYTHPONNSICT 60
 QY 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 DB 61 KCHKGTLYLNDPCPGQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
 QY 121 RDTVCGCRKNQRYHWSENLFCFCNCSICLNGTVHLSQCEKONTVCTCHAGFLENECV 180
 DB 121 RDTVCGCRKNQRYHWSENLFCFCNCSICLNGTVHLSQCEKONTVCTCHAGFLENECV 180
 QY 181 SCSNCKKSECTKCLLPQIENKVGTEDSGTVLLPLVIFGCLSLFLGLMYRYORMK 240
 DB 181 SCSNCKKSECTKCLLPQIENKVGTEDSGTVLLPLVIFGCLSLFLGLMYRYORMK 240
 QY 241 SKLYSIVCGKSTPEKEGEGTTRKPLADNPSFSPPTGFTPLIGSPVSSFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGEGTTRKPLADNPSFSPPTGFTPLIGSPVSSFTSSSTYT 300

```

OY 301 PGDCPNFAAPRRREVAPPYOGADPIATATASDPINPQLQWEDSAHKPOSLOTDDPATLY 360
DB 301 PGDCPNFAAPRRREVAPPYOGADPIATATASDPINPQLQWEDSAHKPOSLOTDDPATLY 360
OY 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPREATLEL 420
DB 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPREATLEL 420
OY 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455

RESULT 3
AAR75084
ID AAR75084 standard; Protein; 455 AA.
XX
AC AAR75084;
XX
DT 19-JAN-1996 (first entry)
XX
DE p55 TNF-R.
XX
KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
KW phorbol myristate acetate; PMA.
XX
OS Homo sapiens.
XX
PH Key
PH Peptide
FT 41..53 Location/Qualifiers
FT /note= "N terminus of soluble p55 TNF-R"
FT Modified-site
FT /note= "glycosylation site"
FT Modified-site
FT /note= "glycosylation site"
FT Modified-site
FT /note= "glycosylation site"
FT Peptide
FT /note= "peptide used in creation of chimeras"
FT Region
FT /note= "spacer region"
FT Misc-difference
FT /note= "major C terminus for soluble p55 TNF-R"
FT Misc-difference
FT /note= "essential for shedding reaction"
FT Misc-difference
FT /note= "minor C terminus for soluble p55 TNF-R"
FT Region
FT /note= "transmembrane region"
XX
XX AU945742-A.
XX
XX 04-MAY-1995.
XX
XX 11-OCT-1994; 94AU-0075742.
XX
XX 12-OCT-1993; 93IL-0107268.
XX
XX (YEDA ) YEDA RES 6 DEV CO LTD.
XX
XX Backin M, Brakebusch C, Varfolomeev E, Wallach D;
XX
XX WPI: 1995-194342/26.
XX
XX N-PSDB; AAG90513.
XX
XX New protease capable of cleaving soluble tumour necrosis factor
XX (TNF) receptor - from cell-bound TNF- receptor; useful for
XX antagonising deleterious effects of TNF.
XX
XX Disclosure: Fig 1; 40pp; English.
XX
XX This sequence represents human p55 tumour necrosis factor (TNF-R).

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```

CC Expression of this receptor is regulated by shedding of the
CC extracellular receptor fragment. The p55 TNF-R can be shed in response
CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC depending on cell type. The only region of the receptor whose structure
CC affects the shedding response is the spacer region (see AAR75012) in the
CC extracellular domain. This region is located close to a site of cleavage
CC of the molecule, and links the Cys rich module to the transmembrane
CC domain. The spacer region of the encoded protein was used to create the
CC chimeras between human p55 TNF-R and murine epidermal growth factor
CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
CC was subjected to deletion mutations (AAR75013-25) and substitutions
CC (AAR75026-47) of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process.
CC The mutations shown in AAR75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
CC inhibitors can be used for enhancing TNF function.
XX
SQ Sequence 455 AA:
Query Match 100.0%; Score 2487; DB 16; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,6e-181;
Matches: 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MGSTVPDLPLVLELAVGIRPSGYTGLVPHLQREKDSVCPQCKYTHPONNSICCT 60
DB 1 MGSTVPDLPLVLELAVGIRPSGYTGLVPHLQREKDSVCPQCKYTHPONNSICCT 60
OY 61 KCHKGTLYNDGCGPGDPTDCRCESGSPFASNNHLRHCSCKREMGQVEISSCTVD 120
DB 61 KCHKGTLYNDGCGPGDPTDCRCESGSPFASNNHLRHCSCKREMGQVEISSCTVD 120
OY 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCNGTVHLSQCRKQNTVCTHAFFLRNECV 180
DB 121 RDTVCGCRKNQYRHYSENLFQCFNCSLCNGTVHLSQCRKQNTVCTHAFFLRNECV 180
OY 181 SCNCKKSLFCTKLCIPQIBNVKGTEDSGTYYLLPIYFPGICLLSLFGLMYRQRMK 240
DB 181 SCNCKKSLFCTKLCIPQIBNVKGTEDSGTYYLLPIYFPGICLLSLFGLMYRQRMK 240
OY 241 SKLYSIVCGKSTPEKGELEGTTKPLAPNPSPTPGFTLGFSPVPSSTSSSTYT 300
DB 241 SKLYSIVCGKSTPEKGELEGTTKPLAPNPSPTPGFTLGFSPVPSSTSSSTYT 300
OY 301 PGDCPNFAAPRRREVAPPYOGADPIATATASDPINPQLQWEDSAHKPOSLOTDDPATLY 360
DB 301 PGDCPNFAAPRRREVAPPYOGADPIATATASDPINPQLQWEDSAHKPOSLOTDDPATLY 360
OY 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPREATLEL 420
DB 361 AVVENVPPLRMKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRTPREATLEL 420
OY 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLGLEDIEBALCGPALPPAPSLLR 455

RESULT 4
AAY30934
ID AAY30934 standard; Protein; 455 AA.
XX
XX AAY30934;
XX
XX 18-OCT-1999 (first entry)
XX
XX Human tumour necrosis factor binding protein.
XX
XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;

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KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KW autoimmune glomerulonephritis; cerebral malaria; immune response;
KW antidiarrhoeal; diagnosis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..29
FT Protein /label= signal_peptide
FT Modified-site 30..455
FT Modified-site 34
FT Modified-site /note= "hypothetical glycosylation site"
FT Modified-site 125
FT Modified-site /note= "hypothetical glycosylation site"
FT Modified-site 131
FT Region /note= "hypothetical glycosylation site"
FT Region 212..230
FT Modified-site /note= "transmembrane region"
FT Modified-site 250
FT Modified-site /note= "hypothetical glycosylation site"
XX
PN EP939121-A2.
XX
PD 01-SEP-1999.
XX
PF 31-AUG-1990; 90EP-0116707.
XX
PR 20-APR-1990; 90CH-0001347.
PR 12-SEP-1989; 89CH-0003319.
PR 08-MAR-1990; 90CH-0000746.
XX
XX (HOEF ) HOFEMANN LA ROCHE & CO AG F.
XX
PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeeger E;
XX
DR WPI: 1999-480840/41.
DR N-PSDB: AA209170.
XX
XX New insoluble proteins, and fragments, that bind to tumor necrosis
XX factor, used to treat e.g. septic shock or cerebral malaria
XX
PS Claim 4a; Fig 1; 25pp; German.
XX
CC This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumor
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence represents
CC a tumor necrosis factor binding protein described in the method of
CC the invention.
XX
SQ Sequence 455 AA:

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Query Match 100.0%; Score 2487; DB 20; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 SCNNCKKSLKCTKLCPLQIENKKGTEDSCTVLLPLVIFFGCLLSLFIGLMYRYQRMK 240
DB 181 SCNNCKKSLKCTKLCPLQIENKKGTEDSCTVLLPLVIFFGCLLSLFIGLMYRYQRMK 240
QY 241 SKLYSTVCGKSTPEKSGELGTTTKPLARNPSPPTGTPPLGSPVSSFTSSSTYT 300
DB 241 SKLYSTVCGKSTPEKSGELGTTTKPLARNPSPPTGTPPLGSPVSSFTSSSTYT 300
QY 301 PGDCPFNAAPREVPAPPYGADPILATALASDPINPVLQKMEDSAHKPOSTLTDPATLY 360
DB 301 PGDCPFNAAPREVPAPPYGADPILATALASDPINPVLQKMEDSAHKPOSTLTDPATLY 360
QY 361 AVVENVPPLRMKEFYVRLGLSDHEIDRLONGRCLEAQAQSLATWRRTTREATLEL 420
DB 361 AVVENVPPLRMKEFYVRLGLSDHEIDRLONGRCLEAQAQSLATWRRTTREATLEL 420
QY 421 IGRVLRMDMLGCLDEDIEFALCGPALPAPSLLR 455
DB 421 IGRVLRMDMLGCLDEDIEFALCGPALPAPSLLR 455

RESULT 5
AAB36266
ID AAB36266 standard; Protein; 455 AA.
XX
AC AAB36266;
XX
DT 20-FEB-2001 (first entry)
XX
DE Human tumour necrosis factor receptor 1.
XX
XX Human; death domain containing receptor; DR3-VI; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO200064465-A1.
XX
PD 02-NOV-2000.
XX
PF 21-APR-2000; 2000WO-US10741.
XX
PR 22-APR-1999; 99US-0130488.
PR 28-MAY-1999; 99US-0136741.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (UNMT) UNITV MICHIGAN.
PA (YUGG/) YU G.
PA (NIJUT/) NI J.
PA (GENTZ/) GENTZ R L.
PA (DILLON/) DILLON P J.
PA (DIXIT/) DIXIT V M.
XX
PI Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX
DR WPI: 2000-687263/67.
XX
PT Treating graft-versus-host disease, cancer, immunodeficiency or an
PT autoimmune disease comprising administering an antibody to Death Domain
PT Containing Receptor proteins and a second therapeutic agent -
XX
PS Disclosure; Fig 3; 273pp; English.
XX
CC The present invention provides the protein and coding sequences for two
CC death domain containing receptors, designated DR3 and DR3-VI. These
CC receptors are involved in apoptosis, and the sequences given can be used
CC in the treatment of cancers, infections, cardiovascular disorders such as
CC arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, emboli
CC and congenital heart defects, neurodegenerative diseases including
CC Alzheimer's and Parkinson's diseases, autoimmune diseases such as multiple
CC sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,

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CC and to promote angiogenesis and wound healing.

XX Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNISICT 60
DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNISICT 60
OY 61 KCHKGTLYNDGPGPGDPTDCRECESSGFASSENHLRHLCSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYNDGPGPGDPTDCRECESSGFASSENHLRHLCSCSKCKREKQVEISSCTVD 120
OY 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
OY 181 SCGNCKKSLLECTKLCPOIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORWK 240
DB 181 SCGNCKKSLLECTKLCPOIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORWK 240
OY 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTIGFSVPSTSTTSSTYT 300
DB 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTIGFSVPSTSTTSSTYT 300
OY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
DB 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
OY 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRRTPRREATLEL 420
DB 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRRTPRREATLEL 420
OY 421 LGRVLRMDLGLCELEDEIEALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLCELEDEIEALCGPALPPAPSLLR 455

RESULT 6

AAB37800 standard; Protein; 455 AA.

AC AAB37800;
DT 23-FEB-2001 (first entry)

DE Human tumour necrosis factor p55 receptor.

XX Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukemia; inflammatory bowel disease.

OS Homo sapiens.

XX MO200064479-A1.

PD 02-NOV-2000.

PF 26-APR-2000; 2000WO-US11700.

PR 27-APR-1999; 99US-0301274.

PA (ANTI-) ANTI BODY SYSTEMS INC.

XX Fredeking TM, Ignatyev GM;

PI
XX WPI: 2000-679646/66.

XX Novel compositions comprising tetracycline or tetracycline-like
PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -
PS Disclosure: Page 167-169; 183pp; English.

CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC systemic sclerosis, inflammatory response associated with trauma,
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease.

SO Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNISICT 60
DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNISICT 60
OY 61 KCHKGTLYNDGPGPGDPTDCRECESSGFASSENHLRHLCSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYNDGPGPGDPTDCRECESSGFASSENHLRHLCSCSKCKREKQVEISSCTVD 120
OY 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDIVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
OY 181 SCGNCKKSLLECTKLCPOIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORWK 240
DB 181 SCGNCKKSLLECTKLCPOIENVKGTEDSGTTVLLPLVIFFGCLLSLFTGLMYRYORWK 240
OY 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTIGFSVPSTSTTSSTYT 300
DB 241 SKIYIVCGKSTPEKGELEGTTTKPLAPNPSPTPGFTIGFSVPSTSTTSSTYT 300
OY 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
DB 301 PGDCPNFAAPRRVAPPYOGADPILATALASDPINPDLQKWEBSAHKPOSIDTDDPATLY 360
OY 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRRTPRREATLEL 420
DB 361 AVVENPPLPWLKKEFVRRLGSDHEIDRLQLONGRCLEAOYSMLATWRRRTPRREATLEL 420
OY 421 LGRVLRMDLGLCELEDEIEALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLGLCELEDEIEALCGPALPPAPSLLR 455

RESULT 7

AAB26984 standard; Protein; 455 AA.

XX AAB26984;

DT 02-FEB-2001 (first entry)

XX Human TNFR 1.

DE Human; TNFR 1; tumour necrosis factor; TNF receptor; immunosuppressive;

KM antiinflammatory; cardiant; antiaesthetic; antidiabetic; antiallergic;
 KM antitubercic; antitubercic; anti-HIV; anticonvulsant; cyostatic;
 KM neuroprotective; gene therapy; Death Domain Containing Receptor 6;
 KM common variable immunodeficiency; X-linked agammaglobulinemia;
 KM severe combined immunodeficiency; Wiskott-Aldrich syndrome;
 KM autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
 KM multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
 KM cardiovascular disease; neurological disease; protein coordinate data.
 XX
 OS Homo sapiens.
 PN WO200056862-A1.
 XX
 XX 28-SEP-2000.
 PD
 XX 16-MAR-2000; 2000WO-US06831.
 PF
 XX 24-MAR-1999; 99US-0126019.
 PR 14-MAY-1999; 99US-0134220.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ni J, Gentz RL, Yu G, Fan P;
 PI
 XX WPI: 2000-594575/56.
 DR
 XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
 PT known as TR9, useful for treating, preventing and diagnosing severe
 PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
 PT and cancer -
 PS Disclosure: Fig 2; 220pp; English.
 XX
 XX The present sequence is TNFR 1, a member of the tumour necrosis factor
 CC receptor family. A novel human tumour necrosis factor receptor,
 CC designated TR9, has been isolated. The TR9 receptor is also known as
 CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
 CC agonists are useful for treating, preventing or diagnosing common
 CC variable immunodeficiency, X-linked agammaglobulinemia, severe combined
 CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
 CC as Rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
 CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
 CC cardiovascular diseases and other neurological diseases.
 CC
 SO Sequence 455 AA;
 Query Match 100.0%; Score 2487; DB 21; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGVPGVIGLVPHLDREKRDVCPQGYIHPONNSICT 60
 DB 1 MGLSTVPDLLPLVLELLVGVPGVIGLVPHLDREKRDVCPQGYIHPONNSICT 60
 QY 61 KCHKSTYLYNOCGPGODPCRECGSFTASENHLRHLSCKRKEGVEISSCTVD 120
 DB 61 KCHKSTYLYNOCGPGODPCRECGSFTASENHLRHLSCKRKEGVEISSCTVD 120
 QY 121 RDTVCGCKRNOYRHYWSENLFQCFNCSICLNGTVHLSCEKONTVCCTGAGFLENCEY 180
 DB 121 RDTVCGCKRNOYRHYWSENLFQCFNCSICLNGTVHLSCEKONTVCCTGAGFLENCEY 180
 QY 121 RDTVCGCKRNOYRHYWSENLFQCFNCSICLNGTVHLSCEKONTVCCTGAGFLENCEY 180
 DB 121 RDTVCGCKRNOYRHYWSENLFQCFNCSICLNGTVHLSCEKONTVCCTGAGFLENCEY 180
 QY 181 SCGNCKSLCTKICLPDIENYKGTEDSGTIVLLPLVIFFGICLLSLFGLMYRYQRWK 240
 DB 181 SCGNCKSLCTKICLPDIENYKGTEDSGTIVLLPLVIFFGICLLSLFGLMYRYQRWK 240
 QY 241 SKLYSIVGKSTPEKEGELETTTKPLAPNPSFSPPTPLGSPVSSFTSSSYT 300
 DB 241 SKLYSIVGKSTPEKEGELETTTKPLAPNPSFSPPTPLGSPVSSFTSSSYT 300
 QY 301 PGDCNFAAPRRREVAAPYOGADPILATALASDPINPPLQKWDASHKPOSLDTPDPAFLY 360
 DB 301 PGDCNFAAPRRREVAAPYOGADPILATALASDPINPPLQKWDASHKPOSLDTPDPAFLY 360

QY 361 AVENVPLRMKEFVRLGLSDHEIDRLQLNGRCUREAYSLATWRRTPREATLEL 420
 DB 361 AVENVPLRMKEFVRLGLSDHEIDRLQLNGRCUREAYSLATWRRTPREATLEL 420
 QY 421 LGRVLRMDLGLCTEDIEFALCPALPPAPSLR 455
 DB 421 LGRVLRMDLGLCTEDIEFALCPALPPAPSLR 455
 RESULT 8
 AAB23446
 ID AAB23446 standard; Protein; 455 AA.
 XX
 XX AAB23446;
 AC
 XX 12-JAN-2001 (first entry)
 DT
 XX Human tumour necrosis factor receptor 1 protein.
 DE
 XX TNFR1; tumour necrosis factor receptor; polymorphism; human;
 KM tumour; cancer; apoptosis; bacterial infection.
 KW
 XX Homo sapiens.
 OS
 XX WO200050436-A1.
 PN
 XX 31-AUG-2000.
 PD
 XX 23-FEB-2000; 2000WO-US04606.
 PF
 XX 23-FEB-1999; 99US-0121314.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (NAND/) NANDABALAN K.
 PA (SCHU/) SCHULZ V P.
 PA (STEP/) STEPHENS J C.
 PA (CHEW/) CHEW A.
 XX
 XX Nandabalan K, Schulz VP, Stephens JC, Chew A;
 DR WPI: 2000-543909/49.
 DR N-PSDB: AAA95105.
 XX
 XX Polynucleotides comprising polymorphic variants of a reference sequence
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
 PT biological function of TNFR1 and identifying drugs targeting the
 PT protein for treating disorders -
 PS Claim 10; Fig 5; 79pp; English.
 XX
 XX The present invention relates to polymorphic variants of the tumour
 CC necrosis factor receptor 1 (TNFR1) gene. The present sequence is
 CC the TNFR1 protein. The sequence of the whole gene is given in AAA95102,
 CC AAA95103 and AAA95104. The polymorphisms were identified by amplifying
 CC and sequencing regions of the gene. Twelve polymorphic loci
 CC were discovered. Of these twelve polymorphisms, four can cause a
 CC change in the TNFR1 protein. The TNFR1 polymorphisms may be useful
 CC for studying the biological function of TNFR1 as well as for
 CC identifying drugs targeting the protein for treatment of disorders
 CC related to its abnormal expression or function such as tumours,
 CC apoptosis related disorders and bacterial infection.
 CC
 SO Sequence 455 AA;
 Query Match 100.0%; Score 2487; DB 21; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.6e-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGVPGVIGLVPHLDREKRDVCPQGYIHPONNSICT 60
 DB 1 MGLSTVPDLLPLVLELLVGVPGVIGLVPHLDREKRDVCPQGYIHPONNSICT 60

QY 61 KCHKGYLYNDGPGDDTDCRECESSFTASENHLRHCLSCSKCKREMOVEISSCTVD 120
 DB 61 KCHKGYLYNDGPGDDTDCRECESSFTASENHLRHCLSCSKCKREMOVEISSCTVD 120
 QY 121 RDTVCCGRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOMTVCHAGFFLRENECV 180
 DB 121 RDTVCCGRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOMTVCHAGFFLRENECV 180
 QY 181 SCGNCKKSLCTCKLCPQIENVKGTEDESGTTVLLPLVIFPGCLLSLFTGLMYRYORWK 240
 DB 181 SCGNCKKSLCTCKLCPQIENVKGTEDESGTTVLLPLVIFPGCLLSLFTGLMYRYORWK 240
 QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLQKWEDESAHKPOSIDTDDPATLY 360
 DB 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLQKWEDESAHKPOSIDTDDPATLY 360
 QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 DB 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 QY 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455

RESULT 9
 ID AAB01336 standard; Protein; 455 AA.
 XX AAB01336;
 AC AAB01336;
 XX 25-SEP-2000 (first entry)
 DT 25-SEP-2000 (first entry)
 XX TNF-R1 death receptor.
 DE TNF-R1 death receptor.
 XX UL14; death receptor; apoptosis; programmed cell death; FAS;
 KM TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
 KM human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200034335-A2.
 PN WO200034335-A2.
 XX 15-JUN-2000.
 PD 15-JUN-2000.
 XX 03-DEC-1999; 99WO-US26035.
 PF 03-DEC-1999; 99WO-US26035.
 XX 04-DEC-1998; 98US-0205018.
 PR 04-DEC-1998; 98US-0205018.
 XX (SCHE) SCHERING CORP.
 PA (SCHE) SCHERING CORP.
 XX Leong C, Phillips JH;
 PI Leong C, Phillips JH;
 XX WPI; 2000-42383/36.
 DR WPI; 2000-42383/36.
 XX Purified or recombinant polypeptide for modulating apoptosis comprises
 PT a sequence which binds to an antibody specific for UL14 or its
 PT fragments
 PS Disclosure; Page 65-67; 76pp; English.
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody
 CC specific for the mature UL14 is useful for screening molecules which
 CC block induction of apoptosis or interfere with antiapoptotic activity.
 CC The polypeptide is also useful for modulating apoptosis and useful in
 CC treatment of conditions associated with abnormal physiology or
 CC development, such as cancer or degenerative conditions and for
 CC regulation of viral infection and replication. At least five
 CC different death receptors are known, which include the CD95

CC (Fas/Apo-1), the TNF receptor-1, TNF receptor apoptosis-mediated
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
 XX Sequence 455 AA:
 SO Sequence 455 AA:
 QY 1 MGISTVPDLPLVLELLVIGTIPSGVIGLVPHLGDEKRDVCPQKTYHPQNNSTICT 60
 DB 1 MGISTVPDLPLVLELLVIGTIPSGVIGLVPHLGDEKRDVCPQKTYHPQNNSTICT 60
 QY 61 KCHKGYLYNDGPGDDTDCRECESSFTASENHLRHCLSCSKCKREMOVEISSCTVD 120
 DB 61 KCHKGYLYNDGPGDDTDCRECESSFTASENHLRHCLSCSKCKREMOVEISSCTVD 120
 QY 121 RDTVCCGRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOMTVCHAGFFLRENECV 180
 DB 121 RDTVCCGRKQYRHYWSENLFQCFNCSLCNGVHLSQCKOMTVCHAGFFLRENECV 180
 QY 181 SCGNCKKSLCTCKLCPQIENVKGTEDESGTTVLLPLVIFPGCLLSLFTGLMYRYORWK 240
 DB 181 SCGNCKKSLCTCKLCPQIENVKGTEDESGTTVLLPLVIFPGCLLSLFTGLMYRYORWK 240
 QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPTPGFTPLGFSVPSTFTSSSTYT 300
 QY 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLQKWEDESAHKPOSIDTDDPATLY 360
 DB 301 PGDCPNFAAPRREYAPPYQADPILATLASDPIPNPLQKWEDESAHKPOSIDTDDPATLY 360
 QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 DB 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRTPPREATLEL 420
 QY 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRMDMLGCLLEDEIEALCGPALPPAPSLLR 455

RESULT 10
 ID AAB86817 standard; Protein; 455 AA.
 XX AAB86817;
 AC AAB86817;
 XX 12-NOV-2001 (first entry)
 DT 12-NOV-2001 (first entry)
 XX Human TNFBP-associated protein #1.
 DE Human TNFBP-associated protein #1.
 XX TNF; tumor necrosis factor binding protein; TNFBP; treatment;
 KM insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
 KM anti-protozoal; treatment; meningococcal sepsis; cerebral malaria;
 KM autoimmune glomerulonephritis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX EP1132471-A2.
 PN EP1132471-A2.
 XX 12-SEP-2001.
 PD 12-SEP-2001.
 XX 31-AUG-1990; 2001EP-0108117.
 PF 31-AUG-1990; 2001EP-0108117.
 XX 12-SEP-1989; 89CH-00003319.
 PR 12-SEP-1989; 89CH-00003319.
 XX 08-MAR-1990; 90CH-0000746.
 PR 08-MAR-1990; 90CH-0000746.
 XX 20-APR-1990; 90CH-0001347.
 PR 20-APR-1990; 90CH-0001347.
 XX 31-AUG-1990; 90EP-0116707.
 PR 31-AUG-1990; 90EP-0116707.
 XX 31-AUG-1990; 99EP-0100703.
 PR 31-AUG-1990; 99EP-0100703.
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlaefer E;
 XX WPI: 2001-559312/63.
 DR N-PSDB; AAH48859.
 XX
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
 XX
 PS Claim 4a; Fig 1; 26pp; German.
 CC This invention describes novel insoluble proteins (I), also their
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antiinflammatory, immunosuppressive, antibacterial,
 CC antiparasitic activity. (I), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis; development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (I), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification
 CC of TNF and for identifying (ant)agonists of TNF. This sequence represents
 CC a human TNF binding protein described in the method of the invention.
 XX
 SQ Sequence 455 AA;

Query Match 100.0%; Score 2487; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4,66-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLDGDRKDSVCPQKGIHQNNISICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLDGDRKDSVCPQKGIHQNNISICT 60
 QY 61 KCHKGTLYLNDGPGQDPTDCRECSGSFTASENHLRHLCSCSKCKEMGOYEISSCTVD 120
 DB 61 KCHKGTLYLNDGPGQDPTDCRECSGSFTASENHLRHLCSCSKCKEMGOYEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECY 180
 DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECY 180
 QY 181 SC5NCKKSLKCTKCLPQLENYKGTEDSGTYVLLPLVIFFGCLSLFLTGIMRYORWK 240
 DB 181 SC5NCKKSLKCTKCLPQLENYKGTEDSGTYVLLPLVIFFGCLSLFLTGIMRYORWK 240
 QY 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFSPPTGFTPLGSPVPSSTFTSSSTYT 300
 DB 241 SKLYSIVCGKSTPEKEGELEGTTRKPLADNPSFSPPTGFTPLGSPVPSSTFTSSSTYT 300
 QY 301 PDDCENFAPRRREVAPRYGADPILATALASDPTRNPLQKWD5AHKPOSLOTDPPATLY 360
 DB 301 PDDCENFAPRRREVAPRYGADPILATALASDPTRNPLQKWD5AHKPOSLOTDPPATLY 360
 QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLONGRCLEA5YMLATWRRRTPRREATLEL 420
 DB 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLONGRCLEA5YMLATWRRRTPRREATLEL 420
 QY 421 IGRVLRMDLGLCLDIEDIEALGPAALPPAPSLR 455
 DB 421 IGRVLRMDLGLCLDIEDIEALGPAALPPAPSLR 455

RESULT 11
 AAB36697
 ID AAB36697 standard; Protein; 455 AA.
 XX
 AC AAB36697;
 XX
 DT 15-MAR-2001 (first entry)
 XX
 DE Human tumour necrosis factor receptor TNFR1 protein Smo ID NO:3.
 XX

KW Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neutrotic;
 KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
 KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
 KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
 KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
 KW apoptotic cell death related disease; autoimmune disorder;
 KW cardiovascular disorder; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200071150-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 18-MAY-2000; 2000WO-US13515.
 XX
 PR 20-MAY-1999; 99US-0135164.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Wei Y, Ruben SM, Gentz RL, NI J;
 XX
 DR WPI: 2001-041051/05.
 XX
 PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or
 PT prevention of cancer, autoimmune disorders and viral infection -
 XX
 PS Disclosure; Fig 2; 285pp; English.

The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain hematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention.

Query Match 100.0%; Score 2487; DB 22; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4,66-181;
 Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLDGDRKDSVCPQKGIHQNNISICT 60
 DB 1 MGISTVPDLLPLVLELLVGIYPSGVIGLVPHLDGDRKDSVCPQKGIHQNNISICT 60
 QY 61 KCHKGTLYLNDGPGQDPTDCRECSGSFTASENHLRHLCSCSKCKEMGOYEISSCTVD 120
 DB 61 KCHKGTLYLNDGPGQDPTDCRECSGSFTASENHLRHLCSCSKCKEMGOYEISSCTVD 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECY 180
 DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCNGTVHLSCEQKONTVCTCHAGFFLENECY 180
 QY 181 SC5NCKKSLKCTKCLPQLENYKGTEDSGTYVLLPLVIFFGCLSLFLTGIMRYORWK 240


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Db 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPLVIFFGICLLSLFLGLMRYORWK 240
QY 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTPGFTPLGFSVPSTFTSSSTYT 300
Db 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTPGFTPLGFSVPSTFTSSSTYT 300
QY 301 PGDCPNFAAPRRVAPPYOGADPLATATLASDPIPNPDLQKWEDESAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPLATATLASDPIPNPDLQKWEDESAHKPOSIDTDDPATLY 360
QY 361 AVVENVPPLMKKEFRVRLGLSDHEIDRLLEONGRCLEAOYSMLATWRRRTPREATLEL 420
Db 361 AVVENVPPLMKKEFRVRLGLSDHEIDRLLEONGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPASLLR 455
Db 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPASLLR 455

RESULT 12
AAB37677
ID AAB37677 standard; protein; 455 AA.
XX
AC AAB37677;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor precursor.
XX
KM TNF inhibitor; antinflammatory; Tumour Necrosis Factor; Interleukin;
XX IL-1; Inflammatory disease; degenerative disease; human.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
PF 19-JAN-1995; 95US-0375242.
XX
PR 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
PA (AMGE-) AMGEN INC.
XX
PI Squites C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannice J, Kohno T;
XX
DR WPI: 2001-006443/01.
DR N-PSDB; AAC83946.
XX
PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
PS Example 6; Fig 21; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the precursor for 30 kDa TNF inhibitor. The 30 kDa
CC TNF inhibitor can inhibit TNF alpha.
XX
SQ Sequence 455 AA;

```

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Best Local Similarity 100.0%; Pred. No. 4 6e-181;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSTVPDLLPLVLELVLGIVPSGVIGLYPHLGDKEKRDVSCPOGKYTHPONNSICCT 60
Db 1 MGSTVPDLLPLVLELVLGIVPSGVIGLYPHLGDKEKRDVSCPOGKYTHPONNSICCT 60
QY 61 KCHKGTLYNDGCPGQDTCRECESSFTASENHLRHCLSCSKRKEKMGQVEISSCTVD 120
Db 61 KCHKGTLYNDGCPGQDTCRECESSFTASENHLRHCLSCSKRKEKMGQVEISSCTVD 120
QY 121 RDTVCCGRKQRYRHYSENLPOCFNCSLCNGYVHLSCOEKONTVCTCHAGFFLRNECV 180
Db 121 RDTVCCGRKQRYRHYSENLPOCFNCSLCNGYVHLSCOEKONTVCTCHAGFFLRNECV 180
QY 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPLVIFFGICLLSLFLGLMRYORWK 240
Db 181 SCSNCKSLCTKLCPLQIENVKGTEDSGTTVLPLVIFFGICLLSLFLGLMRYORWK 240
QY 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTPGFTPLGFSVPSTFTSSSTYT 300
Db 241 SKLYSIVCGKSTPEKEGELGGTTTKPLAPNPSFSPTPGFTPLGFSVPSTFTSSSTYT 300
QY 301 PGDCPNFAAPRRVAPPYOGADPLATATLASDPIPNPDLQKWEDESAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAAPRRVAPPYOGADPLATATLASDPIPNPDLQKWEDESAHKPOSIDTDDPATLY 360
QY 361 AVVENVPPLMKKEFRVRLGLSDHEIDRLLEONGRCLEAOYSMLATWRRRTPREATLEL 420
Db 361 AVVENVPPLMKKEFRVRLGLSDHEIDRLLEONGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPASLLR 455
Db 421 LGRVLRMDLLGCLLEIDIEEALCGPALPAPASLLR 455

RESULT 13
AAB81649
ID AAB81649 standard; protein; 455 AA.
XX
AC AAB81649;
XX
DT 26-SEP-2002 (first entry)
XX
DE Human tumour necrosis factor alpha protein SEQ ID NO:3.
XX
KM Human: apoptosis inducing molecule II; AIM II; cytostatic; antiarthritic;
KM antirheumatic; immunosuppressive; antibacterial; antinflammatory;
KM immunomodulator; vasotropic; protozoacide; cerebroprotective; neoplasia;
KM haematopoiesis regulator; lymphadenopathy; rheumatoid arthritis; HIV;
KM autoimmune disease; graft versus host disease; restenosis; septic shock;
KM cytokine adjuvant; costimulatory molecule; inflammation; bone resorption;
KM cerebral malaria; cachexia.
XX
OS Homo sapiens.
XX
PN US2002064869-A1.
XX
PD 30-MAY-2002.
XX
PF 20-FEB-1998; 98US-0027287.
XX
PR 22-MAR-1996; 96US-013923P.
PR 31-OCT-1996; 96US-030157P.
PR 21-MAR-1997; 97US-0822953.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Yu G, Ruben SM, Ullrich S;
XX
DR WPI: 2002-556723/59.
XX
PT Novel apoptosis inducing molecule II polypeptide useful for treating

```

Query Match 100.0%; Score 2487; DB 22; Length 455;

DB 121 RDYVCGCRKNQRYHYWSENLFQCFNCGLNGTVHLSQOEKONTVCTCHAGFLRENECV 180
 QY 181 SCSNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
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 QY 241 SKLSTYVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 DB 241 SKLSTYVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 QY 301 PGDCPNFAAPRREYAPYOGADPILATLASDPIPNPLQKWEBSAHKPOSIDTDDPATLY 360
 DB 301 PGDCPNFAAPRREYAPYOGADPILATLASDPIPNPLQKWEBSAHKPOSIDTDDPATLY 360
 QY 361 AVVENVPPLRWKEFVRRLGSDHEIDRLONGRCLEAQSMLATWRRRTPRREATLEL 420
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 QY 421 LGRVLRMDLIGCLEDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRMDLIGCLEDEIEALCGPALPPAPSLLR 455

RESULT 15

AA11082 standard; Protein; 455 AA.
 XX AA11082;
 XX 24-MAY-1991 (first entry)
 DE Human 55kD TNF-binding protein.
 KW Tumour Necrosis Factor; binding proteins; septic shock;
 KM auto-immune glomerulonephritis; lymphokine; cytokine.
 XX
 FH key Location/Qualifiers
 FT Modified-site 54
 FT Modified-site 145 /label= putative N-glycosylation site
 FT Modified-site 151 /label= putative N-glycosylation site
 FT Modified-site 270 /label= putative N-glycosylation site
 FT Region 212..230 /label= putative N-glycosylation site
 FT Peptide 1..28 /label= transmembrane region
 FT Peptide /label= signal peptide
 XX
 PN EP417563-A.
 PD 20-MAR-1991.
 XX
 PE 31-AUG-1990; 90EP-0116707.
 XX
 PR 20-APR-1990; 90CH-0001347.
 PR 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 XX
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeger EJ;
 XX
 DR WPT; 1991-081851/12.
 DR N-PSDB; AAO10955.
 XX
 PT Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.
 XX

PS Claim 1; Fig 1; 26pp; German.
 XX
 CC Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AA11072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding
 CC sequence may also contain a fragment encoding a human Ig domain.
 CC Recombinant constructs are used to transform cells to confer
 CC improved TNF-binding properties.
 CC See also AAO10956.
 CC
 XX
 SQ Sequence 455 AA;

Query Match 99.9%; Score 2484; DB 12; Length 455;
 Best Local Similarity 99.8%; Pred. No. 7,7e-181;
 Matches 454; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MGSTVVDLLPLVLELVGTVSGVIGVPHLGDREKRDVCPQCKYIHPQNNISICT 60
 QY 61 KCHKGTLYNDCCPGGDDTCRECESSFTASENHLNCLSCSKRKEKMGVETSSCTVD 120
 DB 61 KCHKGTLYNDCCPGGDDTCRECESSFTASENHLNCLSCSKRKEKMGVETSSCTVD 120
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 DB 121 RDYVCGCRKNQRYHYWSENLFQCFNCGLNGTVHLSQOEKONTVCTCHAGFLRENECV 180
 QY 181 SCSNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
 DB 181 SCSNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
 QY 241 SKLSTYVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 DB 241 SKLSTYVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSSTSTYT 300
 QY 301 PGDCPNFAAPRREYAPYOGADPILATLASDPIPNPLQKWEBSAHKPOSIDTDDPATLY 360
 DB 301 PGDCPNFAAPRREYAPYOGADPILATLASDPIPNPLQKWEBSAHKPOSIDTDDPATLY 360
 QY 361 AVVENVPPLRWKEFVRRLGSDHEIDRLONGRCLEAQSMLATWRRRTPRREATLEL 420
 DB 361 AVVENVPPLRWKEFVRRLGSDHEIDRLONGRCLEAQSMLATWRRRTPRREATLEL 420
 QY 421 LGRVLRMDLIGCLEDEIEALCGPALPPAPSLLR 455
 DB 421 LGRVLRMDLIGCLEDEIEALCGPALPPAPSLLR 455

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 Job time : 42 secs

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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:08:44 ; Search time 12 Seconds
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Title: US-09-899-429a-2

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Gapop 10.0 , Gapext 0.5

Searched: 109717 seqs, 17314136 residues

Total number of hits satisfying chosen parameters: 109717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2487	100.0	US-09-898-234-17	Sequence 17, Appl1
3	2487	100.0	US-09-756-854-5	Sequence 5, Appl1
4	2487	100.0	US-09-899-429a-2	Sequence 2, Appl1
5	2487	100.0	US-09-899-429a-27	Sequence 27, Appl1
6	2487	100.0	US-10-041-574-5	Sequence 5, Appl1
7	2487	100.0	US-09-792-356-2	Sequence 2, Appl1
8	2487	100.0	US-09-792-356-17	Sequence 17, Appl1
9	2487	100.0	US-09-826-212-3	Sequence 3, Appl1
10	2487	100.0	US-09-333-966-5	Sequence 5, Appl1
11	2487	100.0	US-09-027-287-3	Sequence 3, Appl1
12	2487	100.0	US-09-874-138-3	Sequence 3, Appl1
13	2487	100.0	US-09-840-707a-16	Sequence 16, Appl1
14	2487	100.0	US-09-252-6568-3	Sequence 3, Appl1
15	2487	100.0	US-09-899-422-2	Sequence 2, Appl1
16	2487	100.0	US-09-899-422-17	Sequence 17, Appl1
17	2487	100.0	US-09-935-727-5	Sequence 5, Appl1
18	2487	100.0	US-10-005-842-3	Sequence 3, Appl1
19	2487	100.0	US-10-120-397-2	Sequence 2, Appl1

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21	2053	82.5	371	9	US-09-792-356-12	Sequence 12, Appl1
22	2053	82.5	371	10	US-09-899-422-12	Sequence 12, Appl1
23	2039	82.0	371	9	US-09-899-429a-22	Sequence 22, Appl1
24	1550.5	62.3	461	9	US-09-898-234-15	Sequence 15, Appl1
25	1550.5	62.3	461	9	US-09-899-429a-25	Sequence 25, Appl1
26	1550.5	62.3	461	9	US-09-792-356-15	Sequence 15, Appl1
27	1550.5	62.3	461	10	US-09-899-422-15	Sequence 15, Appl1
28	1517	61.0	471	10	US-09-970-532-2	Sequence 2, Appl1
29	1194	48.0	213	9	US-10-125-062-1	Sequence 8, Appl1
30	1192	47.9	211	9	US-09-899-429a-8	Sequence 8, Appl1
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32	1121	45.1	197	9	US-10-112-793-21	Sequence 21, Appl1
33	1117.5	44.9	200	9	US-09-899-429a-12	Sequence 12, Appl1
34	1066.5	42.9	190	9	US-09-899-429a-18	Sequence 18, Appl1
35	1051	42.3	183	9	US-09-899-429a-10	Sequence 10, Appl1
36	1005.5	40.4	336	10	US-09-756-186-8	Sequence 8, Appl1
37	1000	40.2	173	9	US-09-899-429a-16	Sequence 16, Appl1
38	992	39.9	172	9	US-09-899-429a-20	Sequence 20, Appl1
39	979	39.4	285	10	US-09-756-186-6	Sequence 6, Appl1
40	941	37.8	161	9	US-09-898-234-4	Sequence 4, Appl1
41	941	37.8	161	9	US-09-899-429a-4	Sequence 4, Appl1
42	941	37.8	161	10	US-09-792-356-4	Sequence 4, Appl1
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44	941	37.8	161	10	US-09-907-263-2	Sequence 2, Appl1
45	941	37.8	162	9	US-09-899-429a-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-09-898-234-2
; Sequence 2, Application US/09898234
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hummer, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Seratova, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Thsm
; FILER REFERENCE: 98/385-1
; CURRENT APPLICATION NUMBER: US/09/898, 234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525, 998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383, 676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153, 287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821, 750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511, 430
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-898-234-2

Query Match 100.0%; Score 2487; DB 9; Length 455;

Best Local Similarity 100.0%; Pred. No. 4; 9e-158; Mismatches 0; Indels 0; Gaps 0;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPILGDKREKDSVCPQGRYTHPONSICCT 60
OY 61 KCHKGYLYNDGCPGQDTCRCRESGSFPASEHHLRHCISCSKREKQOVERISCTVD 120
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Db      61 KCHKGTLYLNDGPGODPDCRCEGSGFTASBNHLRHCLSCSKCKKMGQVEISSCTVD 120
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Db      121 RDTVCGCRNRQYRHVWSENLFOCFNCSLCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
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Db      181 SCGNCKKSLKCTKRLCPQIENVKGTEDSGTVLPLVIFFGCLLSLFTIGLMYRYQRK 240
QY      241 SKLYSVCKSTPEKEGEGTGTTRKPLAPNPSFSPGFTPLGFSVPVSSFTSSSTYT 300
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Db      241 SKLYSVCKSTPEKEGEGTGTTRKPLAPNPSFSPGFTPLGFSVPVSSFTSSSTYT 300
QY      301 PGDCPNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPSLDTDDPATLY 360
        |||||||
Db      301 PGDCPNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPSLDTDDPATLY 360
QY      361 AVEENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRRTPRRATLTEL 420
        |||||||
Db      361 AVEENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRRTPRRATLTEL 420
QY      421 LGRVLKMDLGLCLDIEEALCGPALPPAPSLLR 455
        |||||||
Db      421 LGRVLKMDLGLCLDIEEALCGPALPPAPSLLR 455

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RESULT 2
US-09-898-234-17
; Sequence 17, Application US/09898234
; Patent No. US2002015512A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: them
; FILE REFERENCE: 98/385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: lnnf-R2
US-09-898-234-17

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Query Match      100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MGLSTVPDLLPLVLYLELLVGYPSGVYGLVPHLDREKRDSVCPQKRYIHQNNISCT 60
        |||||||
Db      1 MGLSTVPDLLPLVLYLELLVGYPSGVYGLVPHLDREKRDSVCPQKRYIHQNNISCT 60
QY      61 KCHKGTLYLNDGPGODPDCRCEGSGFTASBNHLRHCLSCSKCKKMGQVEISSCTVD 120
        |||||||
Db      61 KCHKGTLYLNDGPGODPDCRCEGSGFTASBNHLRHCLSCSKCKKMGQVEISSCTVD 120

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QY      121 RDTVCGCRNRQYRHVWSENLFOCFNCSLCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
        |||||||
Db      121 RDTVCGCRNRQYRHVWSENLFOCFNCSLCLNGTVHLSCEQKONTVCTCHAGFFLRNECV 180
QY      181 SCGNCKKSLKCTKRLCPQIENVKGTEDSGTVLPLVIFFGCLLSLFTIGLMYRYQRK 240
        |||||||
Db      181 SCGNCKKSLKCTKRLCPQIENVKGTEDSGTVLPLVIFFGCLLSLFTIGLMYRYQRK 240
QY      241 SKLYSVCKSTPEKEGEGTGTTRKPLAPNPSFSPGFTPLGFSVPVSSFTSSSTYT 300
        |||||||
Db      241 SKLYSVCKSTPEKEGEGTGTTRKPLAPNPSFSPGFTPLGFSVPVSSFTSSSTYT 300
QY      301 PGDCPNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPSLDTDDPATLY 360
        |||||||
Db      301 PGDCPNFAAPRRVAPRYGADPILATALASDPINPDLQKWDSDAHKPSLDTDDPATLY 360
QY      361 AVEENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRRTPRRATLTEL 420
        |||||||
Db      361 AVEENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEAQSMLATWRRRTPRRATLTEL 420
QY      421 LGRVLKMDLGLCLDIEEALCGPALPPAPSLLR 455
        |||||||
Db      421 LGRVLKMDLGLCLDIEEALCGPALPPAPSLLR 455

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RESULT 3
US-09-756-854-5
; Sequence 5, Application US/09756854
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr3
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentl Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: P#375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-756-854-5

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Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTVPDLLPLVLELVGIVPSGVIGLVPHLGDRKDSVCPQCKYIHQNNISCTT 60
DB 1 MGSTVPDLLPLVLELVGIVPSGVIGLVPHLGDRKDSVCPQCKYIHQNNISCTT 60
QY 61 KCHKGTLYVNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYVNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKCKREKQVEISSCTVD 120
QY 121 RDVYCGCRKQRYHYMSSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
DB 121 RDVYCGCRKQRYHYMSSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
QY 181 SCGNCKKSLCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYQRMK 240
DB 181 SCGNCKKSLCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYQRMK 240
QY 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSFTSSSTYT 300
DB 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSFTSSSTYT 300
QY 301 PGDCPNFAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
DB 301 PGDCPNFAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAQSMLATWRRRTPREATLEL 420
DB 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAQSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGLCLEIDIEELALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLLGLCLEIDIEELALCGPALPPAPSLLR 455

RESULT 4
US-09-899-429a-2
; Sequence 2, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-1
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-429a-2

Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSTVPDLLPLVLELVGIVPSGVIGLVPHLGDRKDSVCPQCKYIHQNNISCTT 60
DB 1 MGSTVPDLLPLVLELVGIVPSGVIGLVPHLGDRKDSVCPQCKYIHQNNISCTT 60
QY 61 KCHKGTLYVNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKCKREKQVEISSCTVD 120
DB 61 KCHKGTLYVNDCCPGPDOTDCRECESSGFTASBNHLRHCLSCSKCKREKQVEISSCTVD 120
QY 121 RDVYCGCRKQRYHYMSSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
DB 121 RDVYCGCRKQRYHYMSSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
QY 181 SCGNCKKSLCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYQRMK 240
DB 181 SCGNCKKSLCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFLIGLWRYQRMK 240
QY 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSFTSSSTYT 300
DB 241 SKLYSTVCGKSTPEKEGELGTTTKPLAPNPSFSPGFTPLGFSVPSSFTSSSTYT 300
QY 301 PGDCPNFAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
DB 301 PGDCPNFAARRREVAPPYOGADPLATALASDPIPNPLOKWEBSAHKPOSLDDDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAQSMLATWRRRTPREATLEL 420
DB 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQNGRCLEAQSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDLLGLCLEIDIEELALCGPALPPAPSLLR 455
DB 421 LGRVLRMDLLGLCLEIDIEELALCGPALPPAPSLLR 455

RESULT 5
US-09-899-429a-27
; Sequence 27, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-1
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
US-09-899-429a-27

Query Match 100.0%; Score 2487; DB 9; Length 455;

Best Local Similarity 100.0%; Pred. NO. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGISTVDPDLLPLVLTLELVGLVIGVPSGVYIGLVPHLGDREKRDSDVCPOKYITHPNNSHICCT	60
Db	1	MGISTVDPDLLPLVLTLELVGLVIGVPSGVYIGLVPHLGDREKRDSDVCPOKYITHPNNSHICCT	60
QY	61	KCHGATYLYNDCCPDPGDDTDCRECESSSFTASENHLRHCLSCSKCKREMOVEISSCTVD	120
Db	61	KCHGATYLYNDCCPDPGDDTDCRECESSSFTASENHLRHCLSCSKCKREMOVEISSCTVD	120
QY	121	RDYCGCRKNQRYHMYSENIFOCNCSLCNGVTHLSOCOKONTVCYCHAGFLRENECV	180
Db	121	RDYCGCRKNQRYHMYSENIFOCNCSLCNGVTHLSOCOKONTVCYCHAGFLRENECV	180
QY	181	SCSNCKRSLECYTKICLPQIENVKGTEDSGTTVLLPLVIFEGICLLSLPIGLMYRYQRMK	240
Db	181	SCSNCKRSLECYTKICLPQIENVKGTEDSGTTVLLPLVIFEGICLLSLPIGLMYRYQRMK	240
QY	241	SKLTSIYCGSTPKBEELBEGTTTKPLAPNPSFSPTGFTPTLGFSPVBSSTTSSTYT	300
Db	241	SKLTSIYCGSTPKBEELBEGTTTKPLAPNPSFSPTGFTPTLGFSPVBSSTTSSTYT	300
QY	301	PGDCPNPAAARRREVAAPYQCADPILATALASDPIPNPLQKEDSAHNPQSLDIDDDPATYX	360
Db	301	PGDCPNPAAARRREVAAPYQCADPILATALASDPIPNPLQKEDSAHNPQSLDIDDDPATYX	360
QY	361	AVVENVPPLMKKEVVRNLGLSDHEIDRLLELQNGRCLEAOYSMLATWRRRTPREATLEI	420
Db	361	AVVENVPPLMKKEVVRNLGLSDHEIDRLLELQNGRCLEAOYSMLATWRRRTPREATLEI	420
QY	421	LGRVLRDMDLIGCLDEIEEALCGPAALPPAPSLLR	455
Db	421	LGRVLRDMDLIGCLDEIEEALCGPAALPPAPSLLR	455

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1      RESULT 6
2      US-10-041-574-5
3      ; Sequence 5, Application US/10041574
4      ; Patent No. US20020168359A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Ni, Jian
7      ; APPLICANT: Yu, Guo-Liang
8      ; APPLICANT: Fan, Ping
9      ; APPLICANT: Gentz, Reiner L.
10     ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
11     ; FILE REFERENCE: PF375p1
12     ; CURRENT APPLICATION NUMBER: US/10/041,574
13     ; CURRENT FILING DATE: 2002-01-10
14     ; PRIOR APPLICATION NUMBER: 09/527,236
15     ; PRIOR FILING DATE: 2000-03-16
16     ; PRIOR APPLICATION NUMBER: 60/052,991
17     ; PRIOR FILING DATE: 1997-06-11
18     ; PRIOR APPLICATION NUMBER: 09/095,094
19     ; PRIOR FILING DATE: 1998-06-10
20     ; PRIOR APPLICATION NUMBER: 60/126,019
21     ; PRIOR FILING DATE: 1999-03-24
22     ; PRIOR APPLICATION NUMBER: 60/134,220
23     ; PRIOR FILING DATE: 1999-05-14
24     ; NUMBER OF SEQ ID NOS: 27
25     ; SOFTWARE: PatentIn Ver. 2.1
26     ; SEQ ID NO 5
27     ; LENGTH: 455
28     ; TYPE: PRT
29     ; ORGANISM: Homo sapiens
30     ; IS-10-041-574-5

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Query Match	100.0%	Score 2487	DB 9	Length 455
Best Local Similarity	100.0%	Pred. No. 4.9e-158		
Matches 455	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MGSTVPDLLPLFVLLELWGIIPSGYIGLVPFHGDREKRSVCPQCKYIHPPNNISCTT	60	

Db	1	MGLSTVDLLPLLVLELLELVG1YPSG5YIG1VPHLHGDEKREKDSVCPQKXTHPQNN5ICT	60
QY	61	KCHGKTYLYNDCBPBGDDTQRCBESSFTASENH1PHCLSCSKCREMOWV1ISCTYD	120
Db	61	KCHGKTYLYNDCBPBGDDTQRCBESSFTASENH1PHCLSCSKCREMOWV1ISCTYD	120
QY	121	RDYVCGGRKNQYRYHWSENLFOCFNC5SLCNGTYHLSCOEKOMTVCC3HAGF1LRENECY	180
Db	121	RDYVCGGRKNQYRYHWSENLFOCFNC5SLCNGTYHLSCOEKOMTVCC3HAGF1LRENECY	180
QY	181	SCSNCKKSLEBTKLC1PQIENWKTBDG5TTVLLPVIYFPGICL5LLE1GLMYRYQRWK	240
Db	181	SCSNCKKSLEBTKLC1PQIENWKTBDG5TTVLLPVIYFPGICL5LLE1GLMYRYQRWK	240
QY	241	SKL5IYCGKSTPEKEBELBGT7TKKPLAHPSPSPMGFP7LIGFSVP5ST7SSSYT	300
Db	241	SKL5IYCGKSTPEKEBELBGT7TKKPLAHPSPSPMGFP7LIGFSVP5ST7SSSYT	300
QY	301	PGDCPNFAAPRREVAAPYOGADPL1LA1ALA5DPI1PN1QWED5AHKPOS1DTPDDPATLY	360
Db	301	PGDCPNFAAPRREVAAPYOGADPL1LA1ALA5DPI1PN1QWED5AHKPOS1DTPDDPATLY	360
QY	361	AVYENVPPLRMKEVRYRLGISDHEIDRLLELQNGRC1REAOYSMLATWRRRTPREATLEL	420
Db	361	AVYENVPPLRMKEVRYRLGISDHEIDRLLELQNGRC1REAOYSMLATWRRRTPREATLEL	420
QY	421	LGRVLRDMDLGCLDEIEEALCGFAAL1PPAPSLLR	455
Db	421	LGRVLRDMDLGCLDEIEEALCGFAAL1PPAPSLLR	455

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RESULT 7
US-09-792-356-2
; Sequence 2, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adelph
; APPLICANT: Maurer-Pogny, Ingrid
; APPLICANT: Strawow, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1997-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-792-356-2

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Query Match	100.0%	Score 2487	DB 9	Length 455
Best Local Similarity	100.0%	Pred. No. 4.9e-158		
Matches 455	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MGSTVDELLPELVLELTVGTPSGVIGLPHLGDREKRSVCPQGYTHPNQNSICT	60	
Db	1	MGSTVDELLPELVLELTVGTPSGVIGLPHLGDREKRSVCPQGYTHPNQNSICT	60	
QY	61	KCHKGTYLNDCCPGPGDTCRECEGSGFTASENHLRHCLSCSKRKMGEVETSSCTVD	120	

Db 61 KCHKGYLVNDGPGODTDCRECESSFTASENHLRHCLSCSKRCKEMGVEISSCTVD 120
QY 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
Db 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
QY 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360
QY 361 AVVENNPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATEL 420
Db 361 AVVENNPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATEL 420
QY 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455
Db 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455

RESULT 8

US-09-792-356-17
; Sequence 17, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Hammler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stracoma, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 17
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
; OTHER INFORMATION: LTNF-R2
US-09-792-356-17

Query Match 100.0%; Score 2487; DB 9; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYTHPONNSICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYTHPONNSICT 60
QY 61 KCHKGYLVNDGPGODTDCRECESSFTASENHLRHCLSCSKRCKEMGVEISSCTVD 120
Db 61 KCHKGYLVNDGPGODTDCRECESSFTASENHLRHCLSCSKRCKEMGVEISSCTVD 120

QY 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
Db 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
QY 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360
QY 361 AVVENNPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATEL 420
Db 361 AVVENNPPLMKKEFVRRLGSDHEIDRLQNGRCLEAOYSMLATWRRRTPREATEL 420
QY 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455
Db 421 LGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455

RESULT 9

US-09-826-212-3
; Sequence 3, Application US/09826212
; Patent No. US20010021516A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488,1280006
; CURRENT APPLICATION NUMBER: US/09/826,212
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-212-3

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4,9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGLSTVPDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCPQCKYTHPONNSICT 60
QY 61 KCHKGYLVNDGPGODTDCRECESSFTASENHLRHCLSCSKRCKEMGVEISSCTVD 120
Db 61 KCHKGYLVNDGPGODTDCRECESSFTASENHLRHCLSCSKRCKEMGVEISSCTVD 120
QY 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
Db 121 RDTVCGCRKNQYRHYSSENLFQCFNCSLCINGTVHLSQCEKONTVCTCHAGFFLRNECV 180
QY 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
Db 181 SCGNCKKSLBCTKLCPLQIENVKGTEDSGTTLPLVIFFGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
Db 241 SKLYSYVCGSKSTPEKEBEGELGTTTKPLAPNPSPTPGFTPLGFSVPSSSTSTYT 300
QY 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360
Db 301 PGDCPNFAARREVPAPYOGADPILATLASDPIPNPLOWKEDSAHKPQSLDTPDPTLY 360

Db 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360
QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420
Db 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420
QY 421 LGRVLKMDLGLCLEDIEBALGCPALPPAPSLR 455
Db 421 LGRVLKMDLGLCLEDIEBALGCPALPPAPSLR 455

RESULT 10
US-09-333-966-5
; Sequence 5, Application US/09333966
; Patent No. US2002009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US2002009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US2002009773A1 Relevant
; TOPOLOGY: No. US2002009773A1 Relevant
; MOLECULE TYPE: protein
; US-09-333-966-5

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLTLLVGIYPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICTT 60
Db 1 MGLSTVPDLLPLVLTLLVGIYPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICTT 60

QY 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCRKENGQVEISSCTVD 120
Db 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCRKENGQVEISSCTVD 120
QY 121 RDTVCGCKRNOYRHWSENLFOCFNCSLCLNGTVHLSCEBKONYCTCAGFFLRENECV 180
Db 121 RDTVCGCKRNOYRHWSENLFOCFNCSLCLNGTVHLSCEBKONYCTCAGFFLRENECV 180
QY 181 SCSNCKKSLECKTKLCPQLENNKGTEDSGTVLLPVIFFGLCLSLPFIGLMTYRORAK 240
Db 181 SCSNCKKSLECKTKLCPQLENNKGTEDSGTVLLPVIFFGLCLSLPFIGLMTYRORAK 240
QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLADNPSPSPPTGFTPLIGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSIVCGKSTPEKEGELGTTTKPLADNPSPSPPTGFTPLIGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360
Db 301 PGDCPFAAPRRREVAAPYOGADPILATASDPINPDLQKWDSSAHKPOSLOTDDPATLY 360
QY 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420
Db 361 AVVENVPPLRMKEFYRRLGLSDHEIDRLQLONGRCILREAOYSMLATWRRTPRREATTLEL 420
QY 421 LGRVLKMDLGLCLEDIEBALGCPALPPAPSLR 455
Db 421 LGRVLKMDLGLCLEDIEBALGCPALPPAPSLR 455

RESULT 11
US-09-027-287-3
; Sequence 3, Application US/09027287A
; Patent No. US20020064869A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Apoptosis Inducing Molecule II
; FILE REFERENCE: 1488, 0650004
; CURRENT APPLICATION NUMBER: US/09/027,287A
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: US 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: US 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: US 60/030,157
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/013,923
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-027-287-3

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLTLLVGIYPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICTT 60
Db 1 MGLSTVPDLLPLVLTLLVGIYPSGVIGLVPHLGDREKRSVCPQGYIHPONNSICTT 60
QY 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCRKENGQVEISSCTVD 120
Db 61 KCHKGTLYLNDGPGQDTPDCRECSGSFTASENHLRHCLSCSKCRKENGQVEISSCTVD 120
QY 121 RDTVCGCKRNOYRHWSENLFOCFNCSLCLNGTVHLSCEBKONYCTCAGFFLRENECV 180
Db 121 RDTVCGCKRNOYRHWSENLFOCFNCSLCLNGTVHLSCEBKONYCTCAGFFLRENECV 180

Db	121	RDVTCGRKNQYHRHWMSENIFQCCNCSLACNGFVHLSQCKQNTWCTCHAGFFLRENECV	180
Qy	181	SCSNCKSLEETKCLCQIENKVTEDBSGTTVLLPLVIFEGCLLSTLFFGLMYRRQRM	240
Db	181	SCSNCKSLEETKCLCQIENKVTEDBSGTTVLLPLVIFEGCLLSTLFFGLMYRRQRM	240
Qy	241	SKLSIVICGKSTPEKEGELGCTTTKPLAPNPSFPNGFFPTLGSFSPVSPSTFTSSSTYV	300
Db	241	SKLSIVICGKSTPEKEGELGCTTTKPLAPNPSFPNGFFPTLGSFSPVSPSTFTSSSTYV	300
Qy	301	PGDCPNPNAARRRVAAPYQCADPLATATLALSDPFPNPLQKWEDSAHKPGSLDTPDPAITLY	360
Db	301	PGDCPNPNAARRRVAAPYQCADPLATATLALSDPFPNPLQKWEDSAHKPGSLDTPDPAITLY	360
Qy	361	AVVENVPPLRMKEFVRRLGSLDHEIDRLTELONGKCLREAGYSMLATVRRTRPREATIEL	420
Db	361	AVVENVPPLRMKEFVRRLGSLDHEIDRLTELONGKCLREAGYSMLATVRRTRPREATIEL	420
Qy	421	LGRLVRMDLGLCLEDIEALCGAALPAPPSLLR	455
Db	421	LGRLVRMDLGLCLEDIEALCGAALPAPPSLLR	455

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RESULT 12
US-09-874-138-3
: Sequence 3, Application US/09874138
: Patent No. US20020072091A1
: GENERAL INFORMATION:
:   APPLICANT: NI, Jian
:   APPLICANT: Gentz, Reinert L.
:   APPLICANT: Yu, Guo-Liang
:   APPLICANT: Rosen, Craig A.
:   TITLE OF INVENTION: Death Domain Containing Receptor 5
:   FILE REFERENCE: 1488.131006
:   CURRENT FILING DATE: 2001-06-06
:   PRIOR APPLICATION NUMBER: 09/565,009
:   PRIOR FILING DATE: 2000-05-04
:   PRIOR APPLICATION NUMBER: 60/146,939
:   PRIOR FILING DATE: 1999-08-13
:   PRIOR APPLICATION NUMBER: 60/133,238
:   PRIOR FILING DATE: 1999-05-07
:   PRIOR APPLICATION NUMBER: 60/132,498
:   PRIOR FILING DATE: 1999-05-04
:   PRIOR APPLICATION NUMBER: 09/042,583
:   PRIOR FILING DATE: 1998-03-17
:   PRIOR APPLICATION NUMBER: 60/054,021
:   PRIOR FILING DATE: 1997-07-29
:   PRIOR APPLICATION NUMBER: 60/040,846
:   PRIOR FILING DATE: 1997-03-17
:   NUMBER OF SEQ ID NOS: 14
:   SOFTWARE: PatentIn Ver. 2.1
:   SEQ ID NO 3
:   LENGTH: 455
:   TYPE: PRT
:   ORGANISM: Homo sapiens
US-09-874-138-3

Query Match      100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pctd. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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Db 1 MGLSTVPDLLPLFLVLTLELVGIPSGVIGLVPHLDRDKRSDVCPQAGKIYHPQNNISICT 60

OY 61 KCHKGTLYLNDPCPGFGQDTCRECHSGSFYASENHLRHCLSCSKCKREMGVIEISCTVD 120
Db 61 KCHKGTLYLNDPCPGFGQDTCRECHSGSFYASENHLRHCLSCSKCKREMGVIEISCTVD 120

OY 121 RDTYCGCKRNOYRIHWSENLFQCFNCSICLNGTVHLSCEQKNFTVCTCHAGFFLRNECV 180
Db 121 RDTYCGCKRNOYRIHWSENLFQCFNCSICLNGTVHLSCEQKNFTVCTCHAGFFLRNECV 180

OY 121 RDTYCGCKRNOYRIHWSENLFQCFNCSICLNGTVHLSCEQKNFTVCTCHAGFFLRNECV 180
Db 121 RDTYCGCKRNOYRIHWSENLFQCFNCSICLNGTVHLSCEQKNFTVCTCHAGFFLRNECV 180

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Qy	181	SCSNCKSLECTKCLPQIENYNGTSDSTVLLPLVIFGCLLSLFIETAMRYGRMK	240
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Db	301	PGDCPNFAARREYAPPYOGADPILTTALASDPINPPLQKWDASHKQSLDTPDPAIY	360
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Db	421	LGRVLRDMDLGCLDEIDIEEALGCPALPLPAPSLIR	455

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	; Sequence 16, Application US/09840707A	
	; Patent No. US20020077276A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Friedeking, Terry M.	
	; APPLICANT: Ignatiev, George M.	
	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS	
	; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS	
	; FILE REFERENCE: 24861-301C	
	; CURRENT APPLICATION NUMBER: US/09/840,707A	
	; CURRENT FILING DATE: 2001-04-23	
	; PRIOR APPLICATION NUMBER: 09/562,979	
	; PRIOR FILING DATE: 2000-04-27	
	; PRIOR APPLICATION NUMBER: 60/1198,210	
	; PRIOR FILING DATE: 1999-04-27	
	; NUMBER OF SEQ ID NOS: 26	
	; SOFTWARE: PatentIn Ver. 2.0	
	; SEQ ID NO 16	
	; LENGTH: 455	
	; TYPE: PRT	
	; ORGANISM: Homo sapiens	
	; FEATURE:	
	; OTHER INFORMATION: Tumor Necrosis Factor p55 Receptor	
	; PUBLICATION INFORMATION:	
	; DATABASE ACCESSION NUMBER: AAA6753/GenBank	
	; DATABASE ENTRY DATE: 1995-08-03	
	US-09-840-707A-16	
	Query Match	100.0%; Score 2487; DB 10; Length 455;
	Best Local Similarity	100.0%; Pred. No. 4,9e-158;
	Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
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Oy	61 KCHKRTYLYNDCPRGGQDTDCRCBCSSGSFTASENLHRLCLSCSKCKRKEGVOEISSCTVD	120
Dd	61 KCHKRTYLYNDCPRGGQDTPDCRCBCSSGSFTASENLHRLCLSCSKCKRKEGVOEISSCTVD	120
Oy	121 RDTYGCGRKNQRYHWSENLFCQFNCISLCNGTVMHLSCQEKONTVCTCIAGFFLRNECV	180
Dd	121 RDTYGCGRKNQRYRWSENLPCFCFNCISLCNGTVMHLSCQEKONTVCTCIAGFFLRNECV	180
Oy	181 SCSNCKKSLECTKLCLPDIENVKGTEDSGTVLPVLVIFFGLCLSLFLIGLMATRYORKM	240
Dd	181 SCSNCKKSLECTKLCLPDIENVKGTEDSGTVLPVLVIFFGLCLSLFLIGLMATRYORKM	240
Oy	241 SKLYSIYCGKSTPEKEGELEGTTTTPLANPSFSPTPGCTPPLGFSVPVSSFTTSSTVT	300
Dd	241 SKLYSIYCGKSTPEKEGELEGTTTTPLANPSFSPTPGCTPPLGFSVPVSSFTTSSTVT	300

Db 241 SKLSTVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGTPPLGFSVPVSSSTFTSSSTYT 300
QY 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360
Db 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360
QY 361 AVENVPPLRKKEFYRRIGLSDEIDRLLELONGRCLREAOYSMLATWRRRTPRRATLEL 420
Db 361 AVENVPPLRKKEFYRRIGLSDEIDRLLELONGRCLREAOYSMLATWRRRTPRRATLEL 420
QY 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455
Db 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455

RESULT 14
US-09-252-656B-3
; Sequence 3, Application US/09252656B
; Patent No. US20020081647A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Zhang, Jun
; APPLICANT: Ullrich, Stephen
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065006
; CURRENT FILING DATE: US/09/252.656B
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: US 60/075,409
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/027,287
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 09/003,886
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 08/822,953
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/013,923
; PRIOR FILING DATE: 1996-03-22
; PRIOR APPLICATION NUMBER: US 60/030,157
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-252-656B-3

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KCHGTYLYNDCPGGQOTDRCESGSGFTASENHLRHCLSCSKCRKMGVEIISCTVD 120
Db 61 KCHGTYLYNDCPGGQOTDRCESGSGFTASENHLRHCLSCSKCRKMGVEIISCTVD 120
QY 121 RDYVCGCKKNQYRHYWSNLFQCFNCSICLNGTYHLSQEQKONTVCCHAGFTLRENECV 180
Db 121 RDYVCGCKKNQYRHYWSNLFQCFNCSICLNGTYHLSQEQKONTVCCHAGFTLRENECV 180
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Db 181 SCNCKKSLLECTKICLPQIENVKGTEDSGTIVLLPVYFFGLCLLSLFTGLMYRYQRMK 240
QY 241 SKLSTVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGTPPLGFSVPVSSSTFTSSSTYT 300
Db 241 SKLSTVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGTPPLGFSVPVSSSTFTSSSTYT 300

QY 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360
Db 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360
QY 361 AVENVPPLRKKEFYRRIGLSDEIDRLLELONGRCLREAOYSMLATWRRRTPRRATLEL 420
Db 361 AVENVPPLRKKEFYRRIGLSDEIDRLLELONGRCLREAOYSMLATWRRRTPRRATLEL 420
QY 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455
Db 421 IGRVLDMDLGCLDIEEALCGPALPAPSLR 455

RESULT 15
US-09-899-422-2
; Sequence 2, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stralowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98.385-H
; CURRENT FILING DATE: US/09/899.422
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 455
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-899-422-2

Query Match 100.0%; Score 2487; DB 10; Length 455;
Best Local Similarity 100.0%; Pred. No. 4.9e-158;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 SCNCKKSLLECTKICLPQIENVKGTEDSGTIVLLPVYFFGLCLLSLFTGLMYRYQRMK 240
Db 181 SCNCKKSLLECTKICLPQIENVKGTEDSGTIVLLPVYFFGLCLLSLFTGLMYRYQRMK 240
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Db 241 SKLSTVCGKSTPEKEGLEGTGTTKPLAPNPSFSPPTGTPPLGFSVPVSSSTFTSSSTYT 300
QY 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360
Db 301 PGDCNFAAPRRVAPPYOGADPILATALASDPINPNLOKWECSAHKPOSLDTPDPAATLY 360

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|||
Db 361 AVVENPPLWKEFVRRLGSDHEIDRLQLONGRCLREAOYMLATWRRRTPPREATLEL 420
|||
Qy 421 LGRVLRDMDLGCLEDEEALCGPALPPAPSLR 455
|||
Db 421 LGRVLRDMDLGCLEDEEALCGPALPPAPSLR 455
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Job time : 13 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 17 Seconds

(without alignments)
787,496 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2487	100.0	455	1	US-08-837-941-2
3	2487	100.0	455	2	US-08-126-016-2
4	2487	100.0	455	4	US-08-815-469-5
5	2487	100.0	455	4	US-09-006-353A-3
6	2487	100.0	455	4	US-09-527-236A-5
7	2487	100.0	455	4	US-08-054-970-2
8	2487	100.0	455	4	US-09-565-918-4
9	2487	100.0	455	4	US-09-573-986-3
10	2482	99.8	455	1	US-08-050-319B-25
11	2482	99.8	455	2	US-08-465-982-25
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13	2463.5	99.1	909	4	US-09-448-868-4
14	2457	98.8	453	4	US-09-086-883A-5
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16	1558	62.6	280	4	US-08-795-445A-46
17	1558	62.6	280	4	US-08-795-447A-46
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20	1558	62.6	280	4	US-08-706-945D-132
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22	1124	45.2	199	1	US-08-050-319B-48
23	1124	45.2	199	2	US-08-465-982-48
24	1121	45.1	197	4	US-08-828-683A-21
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26	1005.5	40.4	336	4	US-08-910-991-8
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28	979	39.4	285	4	US-08-910-991-6	Sequence 6, App11
29	946	38.0	167	1	US-08-050-319B-2	Sequence 2, App11
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33	941	37.8	161	4	US-09-326-39A-2	Sequence 2, App11
34	904	36.3	154	4	US-08-828-683A-12	Sequence 12, App1
35	900	36.2	153	2	US-08-219-237B-4	Sequence 4, App11
36	900	36.2	153	4	US-08-476-862-3	Sequence 12, App1
37	900	36.2	153	4	US-08-476-862-3	Sequence 3, App11
38	900	36.2	153	4	US-08-468-560C-4	Sequence 4, App11
39	873	35.1	154	2	US-08-332-087A-10	Sequence 10, App1
40	861	34.6	307	4	US-08-804-166-4	Sequence 4, App11
41	861	34.6	307	4	US-08-910-991-4	Sequence 4, App11
42	854.5	34.4	158	1	US-08-050-319B-54	Sequence 54, App1
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44	842.5	33.9	256	4	US-08-804-166-2	Sequence 2, App11
45	842.5	33.9	256	4	US-08-910-991-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARTOLOMEEV, Eugene
; APPLICANT: BARKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-668-2
Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8, 9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-837-941-2
; Sequence 2, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEY, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,668
; FILING DATE: 12-OCT-1994
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197

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; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-837-941-2

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Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-20;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 LGRVLRMDLGLCLEDIEBALCGPALPPAPSLLR 455

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RESULT 3
US-08-126-016-2
; Sequence 2, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: NOPAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TNF-I)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/126,016
: FILING DATE: 24-SEP-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/625668
: FILING DATE: 13-DEC-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, ROGER L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 455 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-126-016-2

Query Match      100.0%; Score 2487; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-08-815-469-5
: Sequence 5, Application US/08815469
: Patent No. 6153402
: GENERAL INFORMATION:
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Ni, Jian
: APPLICANT: Dixit, Vishva
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Dillon, Patrick J.
: TITLE OF INVENTION: Death Domain Containing Receptors
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:

```

```

: ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave., NW, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/815,469
: FILING DATE: HERewith
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: No. 6153402 yet Assigned
: FILING DATE: 06-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/028,711
: FILING DATE: 17-OCT-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,285
: FILING DATE: 12-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Steife, Eric K.
: REGISTRATION NUMBER: 36,688
: REFERENCE/DOCKET NUMBER: 1488,0310003/EKS/KRM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 455 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: protein
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US-08-815-469-5

Query Match      100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: 61 KCHKGYLYNDCCPGGDDTDCRECESSFTASENHLRHCLSCSKRKEMGVEISSCTVD 120
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: 241 SKLTSYICGKSTPEKELEGTTTKPLAPNPSFSPGFTPTLGFSPVPSSTFTSSSTYT 300
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: 301 PGDCPNFAAPRRREVAAPYOGADPILATALASDPIPNPLQKWEBSAHKPOSIDTDDPATLY 360
: 361 AVEENVPLRWKEFVRRLGSLDHEIDRLLEONGRCLREAOYSMLATWRRRTPREATLLEL 420
: 361 AVEENVPLRWKEFVRRLGSLDHEIDRLLEONGRCLREAOYSMLATWRRRTPREATLLEL 420
: 361 AVEENVPLRWKEFVRRLGSLDHEIDRLLEONGRCLREAOYSMLATWRRRTPREATLLEL 420
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DB 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLLR 455

RESULT 5
US-09-006-353A-3
; Sequence 3, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-353A-3

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNSICT 60
|||||
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNSICT 60
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DB 361 AVVENVPPLRMKEFVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLLR 455
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DB 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLLR 455

RESULT 6
US-09-527-236A-5
; Sequence 5, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-527-236A-5

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNSICT 60
|||||
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGXIIHPQNSICT 60
QY 61 KKHKGTYLNDPGRGQDTCRECSGSFTASENHLRHCLSCSKCKREKGOVEISSCTVD 120
|||||
DB 61 KKHKGTYLNDPGRGQDTCRECSGSFTASENHLRHCLSCSKCKREKGOVEISSCTVD 120
QY 121 RDTVCGCRKNOYRHYWSENLFCFCNCSICLNGTVHLSCEKONTVCTCAGFELRENECY 180
|||||
DB 121 RDTVCGCRKNOYRHYWSENLFCFCNCSICLNGTVHLSCEKONTVCTCAGFELRENECY 180
QY 181 SCSSNCKKSLCTKCLPQIENVKGTEDSGTVLPLVIFFGCLLSLFTIGLMYRYQRMK 240
|||||
DB 181 SCSSNCKKSLCTKCLPQIENVKGTEDSGTVLPLVIFFGCLLSLFTIGLMYRYQRMK 240
QY 241 SKLIYSIVCGKSTPEKKEGELGTTTKPLAPNPSFSPGFTPLGLSPVPSSTFTSSYTT 300
|||||
DB 241 SKLIYSIVCGKSTPEKKEGELGTTTKPLAPNPSFSPGFTPLGLSPVPSSTFTSSYTT 300
QY 301 PDCPCNFAPRREVAPPYOGADPILATALASDPIPNPLOKMWDSAHKQPSLTDTPATLY 360
|||||
DB 301 PDCPCNFAPRREVAPPYOGADPILATALASDPIPNPLOKMWDSAHKQPSLTDTPATLY 360
QY 361 AVVENVPPLRMKEFVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
|||||
DB 361 AVVENVPPLRMKEFVRLGLSDHEIDRLQLONGRCLEAOYSMLATWRRRTPREATLEL 420
QY 421 LGRVLRMDMLGCLDEDIEEALCGPALPPAPSLLR 455
|||||

Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

RESULT 7
US-08-054-970-2
Sequence 2, Application US/08054970

Patent No. 6395267
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-054-970-2

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDVCPQKXTHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDVCPQKXTHPQNNISICT 60
QY 61 KCHKGTYLYNDGCPGDDTCRCESGFTASENHLRHCLSCSKREKMOVEISSCTVD 120
Db 61 KCHKGTYLYNDGCPGDDTCRCESGFTASENHLRHCLSCSKREKMOVEISSCTVD 120
QY 121 RDVYCGCRKKQRYHYSENLFQCFNCSLCNGTVHLSQCEKQNVCTCHAGFLRENECV 180
Db 121 RDVYCGCRKKQRYHYSENLFQCFNCSLCNGTVHLSQCEKQNVCTCHAGFLRENECV 180
QY 181 SCNSCKSLBCTKLCPLQIENVKGTEDSGTIVLLPLVIFGCLLSLFTGLMYRQRMK 240
Db 181 SCNSCKSLBCTKLCPLQIENVKGTEDSGTIVLLPLVIFGCLLSLFTGLMYRQRMK 240
QY 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAARREVAAPYOGADPLATALASDPIPNPQKWEBSAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAARREVAAPYOGADPLATALASDPIPNPQKWEBSAHKPOSIDTDDPATLY 360

QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
QY 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455
Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

RESULT 8
US-09-565-918-4
Sequence 4, Application US/09565918

Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.130005
CURRENT APPLICATION NUMBER: US/09/565,918
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-4

Query Match 100.0%; Score 2487; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 8.9e-203;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDVCPQKXTHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDVCPQKXTHPQNNISICT 60
QY 61 KCHKGTYLYNDGCPGDDTCRCESGFTASENHLRHCLSCSKREKMOVEISSCTVD 120
Db 61 KCHKGTYLYNDGCPGDDTCRCESGFTASENHLRHCLSCSKREKMOVEISSCTVD 120
QY 121 RDVYCGCRKKQRYHYSENLFQCFNCSLCNGTVHLSQCEKQNVCTCHAGFLRENECV 180
Db 121 RDVYCGCRKKQRYHYSENLFQCFNCSLCNGTVHLSQCEKQNVCTCHAGFLRENECV 180
QY 181 SCNSCKSLBCTKLCPLQIENVKGTEDSGTIVLLPLVIFGCLLSLFTGLMYRQRMK 240
Db 181 SCNSCKSLBCTKLCPLQIENVKGTEDSGTIVLLPLVIFGCLLSLFTGLMYRQRMK 240
QY 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSPTGFTPTLGFSPVPSSTFTSSSTYT 300
Db 241 SKLYSTYCGSTPEKEBELGTTTKPLAPNPSPTGFTPTLGFSPVPSSTFTSSSTYT 300
QY 301 PGDCPNFAARREVAAPYOGADPLATALASDPIPNPQKWEBSAHKPOSIDTDDPATLY 360
Db 301 PGDCPNFAARREVAAPYOGADPLATALASDPIPNPQKWEBSAHKPOSIDTDDPATLY 360
QY 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
Db 361 AVVENVPPLMKKEFVRRLGSDHEIDRLQLONGRCLEADQYSLMATWRRTTTPREATLEL 420
QY 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455
Db 421 LGRVLRMDLLGCLDEIEEALCGPALPPAPSLLR 455

Db 421 LGRVLRMDLGLCLEDIEEALCGPALPPAPSLR 455

RESULT 9

US-09-573-986-3

Sequence 3, Application US/09573986

Patent No. 6455040

GENERAL INFORMATION:

APPLICANT: Wei, Yang-Fei

APPLICANT: Ni, Jian

APPLICANT: Gentz, Reiner

APPLICANT: Ruben, Steven

TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

FILE REFERENCE: 1488.1280004

CURRENT APPLICATION NUMBER: US/09/573,986

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 455

TYPE: PRT

ORGANISM: Homo sapiens

US-09-573-986-3

Query Match

Best Local Similarity 100.0%; Score 2487; DB 4; Length 455;

Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPONNSICT 60

DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPONNSICT 60

QY 61 KHKGTYYLNDGPGGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120

DB 61 KHKGTYYLNDGPGGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120

QY 121 RPTVGGCRKNQRYHWSENLFCQFNCISLNGTVHLSQOEKQNTVCTCHAGFLENECY 180

DB 121 RPTVGGCRKNQRYHWSENLFCQFNCISLNGTVHLSQOEKQNTVCTCHAGFLENECY 180

QY 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYVLLPVIFFGCLSLFLIGLMRYORMK 240

DB 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYVLLPVIFFGCLSLFLIGLMRYORMK 240

QY 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNBSFSPGFTPLGFSVPVSSFTSSSTYT 300

DB 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNBSFSPGFTPLGFSVPVSSFTSSSTYT 300

QY 301 PGDCNFAAPREVAAPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360

DB 301 PGDCNFAAPREVAAPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360

QY 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRTPRREATLEL 420

DB 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRTPRREATLEL 420

QY 421 LGRVLRMDLGLCLEDIEEALCGPALPPAPSLR 455

DB 421 LGRVLRMDLGLCLEDIEEALCGPALPPAPSLR 455

RESULT 10

US-08-050-319B-25

Sequence 25, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,319B

FILING DATE: 10-May-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Robbins, Roberta L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 5150-0030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999

TELEFAX: (415) 327-3231

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-050-319B-25

Query Match

Best Local Similarity 99.8%; Score 2482; DB 1; Length 455;

Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPONNSICT 60

DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPONNSICT 60

QY 61 KHKGTYYLNDGPGGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120

DB 61 KHKGTYYLNDGPGGQDTCRECSGSFTASENHLRHCLSCSKCKEMGOVEISSCTVD 120

QY 121 RPTVGGCRKNQRYHWSENLFCQFNCISLNGTVHLSQOEKQNTVCTCHAGFLENECY 180

DB 121 RPTVGGCRKNQRYHWSENLFCQFNCISLNGTVHLSQOEKQNTVCTCHAGFLENECY 180

QY 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYVLLPVIFFGCLSLFLIGLMRYORMK 240

DB 181 SCSNCKKSELECTKLCPLQIENYKGTEDSGTYVLLPVIFFGCLSLFLIGLMRYORMK 240

QY 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNBSFSPGFTPLGFSVPVSSFTSSSTYT 300

DB 241 SKLYSIYVGKSTPEKEGELGTTTKPLAPNBSFSPGFTPLGFSVPVSSFTSSSTYT 300

QY 301 PGDCNFAAPREVAAPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360

DB 301 PGDCNFAAPREVAAPYOGADPILATLASDPIPNPLOKWDNSAHKQSLDTPDPTLY 360

QY 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRTPRREATLEL 420

DB 361 AVVENVPLRMKEFYRRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRRTPRREATLEL 420

QY 421 LGRVLRMDLGLCLEDIEEALCGPALPPAPSLR 455

DB 421 LGRVLRMDLGLCLEDIEEALCGPALPPAPSLR 455

RESULT 11

US-08-465-982-25

Sequence 25, Application US/08465982

Patent No. 5863786

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

;; TITLE OF INVENTION: Modified human TNFalpha (Tumor
;; NUMBER OF INVENTION: Necrosis Factor alpha) Receptor
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Reed & Robbins
;; STREET: 635 Bryant Street
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94301
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/465,982
;; FILING DATE:
;; CLASSIFICATION:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US/08/050,319
;; FILING DATE: 10-May-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Robbins, Roberta L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 5150-0030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 455 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-465-982-25
;
Query Match 99.8%; Score 2482; DB 2; Length 455;
Best Local Similarity 99.8%; Pred. No. 2,4e-202;
Matches 454; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSTVPDLPLVLELLVIGTIPSGVIGLVPHLGDREKRDVCPQKTYHPONNSICT 60
DB 1 MGSTVPDLPLVLELLVIGTIPSGVIGLVPHLGDREKRDVCPQKTYHPONNSICT 60
QY 61 KCHKGTLYNDGCGPGDTCRCESGSPYASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
DB 61 KCHKGTLYNDGCGPGDTCRCESGSPYASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
QY 121 RDVTGCGRRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENECV 180
DB 121 RDVTGCGRRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENECV 180
QY 181 SCNSCKKSLCTKLCIPQLEINVKGTEDSGTIVLLPVIFFGICLSLFTGLMYRYQRW 240
DB 181 SCNSCKKSLCTKLCIPQLEINVKGTEDSGTIVLLPVIFFGICLSLFTGLMYRYQRW 240
QY 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPTLGFSPVSSSTSTYT 300
DB 241 SKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPTLGFSPVSSSTSTYT 300
QY 301 PGDCPNAPRREYAPPYQADPLATATLASDPLPNPLQKWEDSAHKPOSIDDDPATLY 360
DB 301 PGDCPNAPRREYAPPYQADPLATATLASDPLPNPLQKWEDSAHKPOSIDDDPATLY 360
QY 361 AVVENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEADQSMATYRRRRTPREATLEL 420
DB 361 AVVENVPLRMKEFVRRLGSDHEIDRLQLONGRCLEADQSMATYRRRRTPREATLEL 420
QY 421 LGRVLRMDMLGCLIEDIEALCGPAALPPAPSLLR 455
DB 421 LGRVLRMDMLGCLIEDIEALCGPAALPPAPSLLR 455

RESULT 12
US-09-013-895A-4
; Sequence 4, Application US/09013895A
; Patent No. 6342363
;; GENERAL INFORMATION:
;; APPLICANT: NI, Jian
;; APPLICANT: Rosen, Craig A.
;; APPLICANT: Pan, James G.
;; APPLICANT: Gentz, Reiner L.
;; APPLICANT: Dixit, Vishva M.
;; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
;; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
;; STREET: 9410 KEY WEST AVENUE
;; CITY: ROCKVILLE
;; STATE: MD
;; COUNTRY: US
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/013,895A
;; FILING DATE: 27-JAN-1998
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1300002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 909 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-013-895A-4
;
Query Match 99.1%; Score 2463.5; DB 4; Length 909;
Best Local Similarity 99.3%; Pred. No. 2.2e-200;
Matches 453; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGSTVPDLPLVLELLVIGTIPSGVIGLVPHLGDREKRDVCPQKTYHPONNSICT 60
DB 454 MGSTVPDLPLVLELLVIGTIPSGVIGLVPHLGDREKRDVCPQKTYHPONNSICT 513
QY 61 KCHKGTLYNDGCGPGDTCRCESGSPYASENHLRHCLSCSKCRKEMGOVEISSCTV 119
DB 61 KCHKGTLYNDGCGPGDTCRCESGSPYASENHLRHCLSCSKCRKEMGOVEISSCTV 119
QY 120 DRDTVCGCRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENEC 179
DB 120 DRDTVCGCRKQYRHYWSENLFQCFNCSLCINGVHLSCEKONTVCTCHAGFFLRENEC 179
QY 180 VSCNSCKKSLCTKLCIPQLEINVKGTEDSGTIVLLPVIFFGICLSLFTGLMYRYQRW 239
DB 634 VSCNSCKKSLCTKLCIPQLEINVKGTEDSGTIVLLPVIFFGICLSLFTGLMYRYQRW 633
QY 240 KSKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPTLGFSPVSSSTSTYT 299
DB 694 KSKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFSPPTGFTPTLGFSPVSSSTSTYT 753
QY 300 TPDDCPFAAPRREYAPPYQADPLATATLASDPLPNPLQKWEDSAHKPOSIDDDPATLY 359
DB 300 TPDDCPFAAPRREYAPPYQADPLATATLASDPLPNPLQKWEDSAHKPOSIDDDPATLY 359

Db 754 TPGDCNFAAPRREVAAPYOGADPILATALASDPINPLQKWDASHKQSDTDDPATL 813
QY 360 YAVENVPPLRKKEFYRRIGLSDEIDRELONGRCLREAOYSMLATWRRRPPREATLE 419
Db 814 YAVENVPPLRKKEFYRRIGLSDEIDRELONGRCLREAOYSMLATWRRRPPREATLE 873
QY 420 LIGRVLKMDLGLCLEDIEALCGPALPPAPSLR 455
Db 874 LIGRVLKMDLGLCLEDIEALCGPALPPAPSLR 909

RESULT 13

US-09-448-868-4
; Sequence 4, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (Ap02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 909 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-448-868-4

Query Match 99.1%; Score 2463.5; DB 4; Length 909;
Best Local Similarity 99.3%; Pred. No. 2.2e-200;
Matches 453; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGLSTVPPDLLPLVLLLELVGITYPSGVIGLVPHLGDRKRDVSCPOGKYTHPNNISICT 60
Db 454 MGLSTVPPDLLPLVLLLELVGITYPSGVIGLVPHLGDRKRDVSCPOGKYTHPNNISICT 513
QY 61 KCHKSTYLYNDGPGGQDTCRECESSGFTASENHLRHCLSCSKCR-KEMGOVEISSCTV 119
Db 514 KCHKSTYLYNDGPGGQDTCRECESSGFTASENHLRHCLSCSKCRKEMGOVEISSCTV 573

QY 120 DRDTVCGCKRKNQYRHYSENLFQCFNCISCLNGTVHLSCQEQKNYVCTCHAGFELRENEC 179
Db 574 DRDTVCGCKRKNQYRHYSENLFQCFNCISCLNGTVHLSCQEQKNYVCTCHAGFELRENEC 633
QY 180 VSCSNCKKLECKTCLCPLENNKVGTEDESGTTLPLVTFEFGCLSLFLGIMRYORW 239
Db 634 VSCSNCKKLECKTCLCPLENNKVGTEDESGTTLPLVTFEFGCLSLFLGIMRYORW 693
QY 240 KSKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFPTPGFTPLGFSVPSSFTSSSTY 299
Db 694 KSKLYSIVCGKSTPEKEGELGTTTKPLAPNPSFPTPGFTPLGFSVPSSFTSSSTY 753
QY 300 TPGDCNFAAPRREVAAPYOGADPILATALASDPINPLQKWDASHKQSDTDDPATL 359
Db 754 TPGDCNFAAPRREVAAPYOGADPILATALASDPINPLQKWDASHKQSDTDDPATL 813
QY 360 YAVENVPPLRKKEFYRRIGLSDEIDRELONGRCLREAOYSMLATWRRRPPREATLE 419
Db 814 YAVENVPPLRKKEFYRRIGLSDEIDRELONGRCLREAOYSMLATWRRRPPREATLE 873
QY 420 LIGRVLKMDLGLCLEDIEALCGPALPPAPSLR 455
Db 874 LIGRVLKMDLGLCLEDIEALCGPALPPAPSLR 909

RESULT 14

US-09-086-483A-5
; Sequence 5, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PP379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-5

Query Match 98.8%; Score 2457; DB 4; Length 453;
Best Local Similarity 99.6%; Pred. No. 3,1e-200;
Matches 453; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNSICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNSICT 58
QY 61 KCHKGYLYNDPCPGQDTPDCRECESSGFPASENHLRHCLSCSKRKMGMQVEIISCTVD 120
DB 59 KCHKGYLYNDPCPGQDTPDCRECESSGFPASENHLRHCLSCSKRKMGMQVEIISCTVD 118
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 119 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 178
QY 181 SCNCKKSLECTKLCLOIENVKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
DB 179 SCNCKKSLECTKLCLOIENVKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 238
QY 241 SKLYSIVCGKSTPEKEGELBEGTTTKPLAPNPSFSPPTGFTPLGFSPPVSSFTTSSSTYT 300
DB 239 SKLYSIVCGKSTPEKEGELBEGTTTKPLAPNPSFSPPTGFTPLGFSPPVSSFTTSSSTYT 298
QY 301 PGDDPNFAAPRREYAAPRYQADPILATNALASDPIPNPLQKEDSAHKRQSDTDDPATLY 360
DB 299 PGDDPNFAAPRREYAAPRYQADPILATNALASDPIPNPLQKEDSAHKRQSDTDDPATLY 358
QY 361 AVENVPPLRKKEFYVRRLGSDHEIDRLONGRCLREAOYSMLATWRPRRREATLEL 420
DB 359 AVENVPPLRKKEFYVRRLGSDHEIDRLONGRCLREAOYSMLATWRPRRREATLEL 418
QY 421 LGRVLRDMDLLGCLIEDIEALCGPALPPAPSLLR 455
DB 419 LGRVLRDMDLLGCLIEDIEALCGPALPPAPSLLR 453

RESULT 15
US-08-974-022-46
Sequence 46, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-46

Query Match 62.6%; Score 1558; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.4e-124;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNSICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQCKYIHPONNSICT 60
QY 61 KCHKGYLYNDPCPGQDTPDCRECESSGFPASENHLRHCLSCSKRKMGMQVEIISCTVD 120
DB 61 KCHKGYLYNDPCPGQDTPDCRECESSGFPASENHLRHCLSCSKRKMGMQVEIISCTVD 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGCRKNQYRHYWSENLFQCFNCISCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
QY 181 SCNCKKSLECTKLCLOIENVKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
DB 181 SCNCKKSLECTKLCLOIENVKGTEDSGTTLPLVIFPGCLLSLFTGLMYRYORWK 240
QY 241 SKLYSIVCGKSTPEKEGELBEGTTTKPLAPNPSFSPPTGFT 280
DB 241 SKLYSIVCGKSTPEKEGELBEGTTTKPLAPNPSFSPPTGFT 280

Search completed: December 27, 2002, 15:09:03
Job time: 19 secs

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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 21 Seconds

(without alignments)
2082.912 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGISTVPDLLPLVLELLV.....DIEALGPALPPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2487	100.0	455	1 GQHUT1	tumor necrosis fac
2	1738	69.9	461	2 JC4302	tumor necrosis fac
3	1563.5	62.9	461	1 GORRT1	tumor necrosis fac
4	1521	61.2	454	1 GOMST1	tumor necrosis fac
5	251.5	10.1	435	2 IS4182	tumor necrosis fac
6	240.5	9.7	427	1 GQHUN	tumor necrosis fac
7	223	9.0	425	1 A26431	nerve growth facto
8	205	8.2	474	2 B38634	tumor necrosis fac
9	204.5	8.2	459	2 I48854	gene murine tumour
10	200	8.0	326	1 GQVZML	72 protein - myxom
11	196.5	7.9	416	1 UN0006	nerve growth facto
12	192	7.7	325	2 B43692	72 protein - rabbi
13	189.5	7.6	327	2 A46484	apoptosis-mediatin
14	186.5	7.5	651	2 JC7705	death receptor-6 -
15	183.5	7.4	461	1 A35356	tumor necrosis fac
16	177	7.1	335	2 A40036	apoptosis-mediatin
17	176.5	7.1	305	2 A46476	B cell-associated
18	174	7.0	324	2 JC2395	B cell antigen precu
19	166.5	6.7	277	2 A60771	B-cell activation
20	166.5	6.7	349	2 D72175	G2R protein - vari
21	164	6.6	348	2 T28623	hypothetical prote
22	164	6.6	349	2 D36858	gene GAR protein -
23	158	6.4	260	1 A46517	CD27 antigen precu
24	157.5	6.3	314	2 I37383	FAS soluble protei
25	154.5	6.2	355	2 A42086	CD30 antigen precu
26	154	6.2	677	2 C42125	trophozoite cytol
27	148	6.0	1548	2 S34583	serine proteinase
28	145.5	5.9	837	2 S43566	furin (EC 3.4.21.7
29	143.5	5.8	1680	2 A43434	furin (EC 3.4.21.7

30	143	5.7	250	1 A49053	CD27 antigen precu
31	140	5.6	2824	2 T22759	hypothetical prote
32	136.5	5.5	272	2 I48700	gene ox40 protein
33	133.5	5.4	271	2 S12783	OX40 antigen precu
34	132.5	5.3	899	2 G02428	subtilisin-like pr
35	132.5	5.3	915	2 JC6148	subtilisin-like pr
36	131.5	5.3	826	2 A60385	monocyte surface a
37	130.5	5.2	3672	2 T23433	hypothetical prote
38	130.5	5.2	3704	2 T37316	probable laminin a
39	126.5	5.1	728	2 A48830	hypothetical prote
40	124.5	5.0	277	2 I37552	OX40 homolog - hum
41	124	5.0	468	2 S26741	T-cell glycoprotei
42	124	5.0	884	2 T18649	hypothetical prote
43	122.5	4.9	192	2 T25513	hypothetical prote
44	122.5	4.9	213	2 S25647	ookinete surface p
45	121.5	4.9	1299	2 T43251	furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1
GOHUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N/Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N/Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000
C/Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; J0758; A60231;
R/Fuchs, P.; Strehl, S.; Dvorzak, M.; Hummler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A/Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to
A/Reference number: A38208; MUID:92250049; PMID:1315717
A/Accession: A38208
A/Molecule type: DNA
A/Residues: 1-455 <PUC>
A/Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R/Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tachuchi, H.; Less
Cell 61, 351-359, 1990
A/Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A/Reference number: A34899; MUID:90235284; PMID:2158862
A/Accession: A34899
A/Molecule type: mRNA
A/Residues: 1-455 <LOE>
A/Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A/Experimental source: Placenta
A/Note: part of this sequence, including the amino end of the mature protein, confirm
R/Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A/Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A/Reference number: A34900; MUID:90235285; PMID:2158863
A/Accession: A34900
A/Molecule type: mRNA
A/Residues: 1-455 <SCH>
A/Cross-references: GB:A33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R/Hummler, A.; Maurer-Fogy, I.; Kroecke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A/Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A/Reference number: A36555; MUID:91090841; PMID:1702293
A/Accession: A36555
A/Molecule type: mRNA
A/Residues: 1-455 <HIM>
A/Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A/Accession: C36555
A/Molecule type: protein
A/Residues: 30-38;41-53; 'X',55-79; 'XX',82-94; 'NK', 'XX',100-104;107-128;162-167; 'X',16
A/Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R/Gray, P.W.; Barrett, K.; Chantley, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A/Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A/Reference number: A38281; MUID:910121509; PMID:2170974
A/Accession: A38281
A/Molecule type: mRNA

A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R.Noplat, Y.; Kemper, O.; Bräkebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Hollmann
EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
I form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NOP>
A:Cross-references: EMBL:X55133; NID:g37223; PIDN:CAA39021.1; PID:g37224
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R.Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: J70758; MUID:94085779; PMID:8263379
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
R.Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R.Gatnaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R.Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OIS>
A:Experimental source: renal failure patient urine
R.Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
A.Kirihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: J2404; MUID:95128033; PMID:7765720
A:Accession: J2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 2487; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 8,66-159;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGISTVPDILLPLVILELLVGIYPSGVILVPHLGDREKRDSCPGKTIHQNNISCTT 60
|||||
Db 1 MGISTVPDILLPLVILELLVGIYPSGVILVPHLGDREKRDSCPGKTIHQNNISCTT 60
|||||
QY 61 KCHKGTLYLNDPCPGPDTRCECESGSFTASENHRLHCLSCSKCKEMGOYEISSCTVD 120
|||||
Db 61 KCHKGTLYLNDPCPGPDTRCECESGSFTASENHRLHCLSCSKCKEMGOYEISSCTVD 120
|||||
QY 121 RPTVCGCRNNOYRHYWSENLFCFNCSLCLNGTVHLSCQEKONTVCTCHAGFFLRENECV 180
|||||
Db 121 RPTVCGCRNNOYRHYWSENLFCFNCSLCLNGTVHLSCQEKONTVCTCHAGFFLRENECV 180
|||||
QY 181 SCGNCKSLIECTKRLCLPQLENNKGFDSSTYVILPLVIFFGCLLSLFTGLMYRQRMK 240
|||||
Db 181 SCGNCKSLIECTKRLCLPQLENNKGFDSSTYVILPLVIFFGCLLSLFTGLMYRQRMK 240
|||||
QY 241 SKLYSVCKSPKPEKGELEGTTTKPLAPNPSRPPGPTPLGFSVPSSFTSSSTYT 300
|||||
Db 241 SKLYSVCKSPKPEKGELEGTTTKPLAPNPSRPPGPTPLGFSVPSSFTSSSTYT 300
|||||
QY 301 PEDCPNFAPRRREVAPPYOGADPILATLASDPINPILQKWDSDAHKPSQDTPDPAATLY 360
|||||
Db 301 PEDCPNFAPRRREVAPPYOGADPILATLASDPINPILQKWDSDAHKPSQDTPDPAATLY 360
|||||
QY 361 AVEENVPPLRMKEFVARRLSDHEIDRLQRCRLRENOYMLATWRRRTRENTLEL 420
|||||
Db 361 AVEENVPPLRMKEFVARRLSDHEIDRLQRCRLRENOYMLATWRRRTRENTLEL 420
|||||
QY 421 LGRVLKMDLCLDEIDIEALGPAALPPAPSLR 455
|||||
Db 421 LGRVLKMDLCLDEIDIEALGPAALPPAPSLR 455
|||||

RESULT 2
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AMC40499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SUT>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NGI>
F:84-126/Domain: NGF receptor repeat homology <NGF>
F:211-231/Domain: transmembrane #status predicted <TM>
F:361-447/Domain: signal transduction #status predicted <ST>

F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.9%; Score 1738; DB 2; Length 461;

Best Local Similarity 71.6%; Pred. No. 9e-109;

Matches 331; Conservative 29; Mismatches 94; Indels 8; Gaps 4;

```

QY 1 MGSTVPDLLPLVLELLVGYIGVPSYIGLVPHLCBDEKRDSCVPOCKYTHPONNSICTT 60
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Db 1 MGSTVPGLLPLVLRALVDVYPAGVHGLVHPGDRKREKESLCPOCKYSHPNRSICTT 60
QY 61 KCHKGYLYNDCEPGDGTCCRECEGSPFASENLHRLHSCSKCKREMGVEISSCTVD 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 KCHKGYLYNDCEPGDGTCCRECEGSPFASENLHRLHSCSKCKREMGVEISSCTVD 120
QY 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
QY 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
QY 181 SCNSCKKSLSECTKICLPQIENWKTEDSGTTLVPLVIFPGCLLSLFTGLMRYGRWK 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 SCNSCKKSLSECTKICLPQIENWKTEDSGTTLVPLVIFPGCLLSLFTGLMRYGRWK 240
QY 241 SKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 SKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
QY 240 PKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 PKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
QY 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
QY 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
QY 354 DDPAATLYAVENVPLRMKEFVRRLGLSDHEIDRLQNGRCLEAOYSMLATWRRTPR 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 354 DDPAATLYAVENVPLRMKEFVRRLGLSDHEIDRLQNGRCLEAOYSMLATWRRTPR 413
QY 360 ADPAATLYAVVDGVPTRMKFEVRRLGLSEHEIERLELQNGRCLEAOYSMLAEWRRTRSR 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 ADPAATLYAVVDGVPTRMKFEVRRLGLSEHEIERLELQNGRCLEAOYSMLAEWRRTRSR 419
QY 414 REATLELGRVLRMDLGLCLEDIEEALCGPALPAPSLR 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 REATLELGRVLRMDLGLCLEDIEEALCGPALPAPSLR 461

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RESULT 3

GOMST1
tumor necrosis factor receptor 1 precursor - rat
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C:Accession: B36555
R:Hummer, A.; Maurer-Fogy, I.; Kroecke, M.; Scheurich, P.; Pfizenmaier, K.; Lant, M.;
DNA Cell Biol. 9: 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <IHM>
A:Cross-references: GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/DNA: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/DNA: extracellular #status predicted <EX>
F:30-201/Product: tumor necrosis factor binding protein #status predicted <TBP>
F:44-84/DNA: NGF receptor repeat homology <NG1>
F:84-167/DNA: NGF receptor repeat homology <NG2>
F:127-167/DNA: NGF receptor repeat homology <NG3>
F:168-204/DNA: NGF receptor repeat homology <NG4>
F:212-234/DNA: transmembrane #status predicted <MEM>
F:235-461/DNA: intracellular #status predicted <INT>
F:34,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.9%; Score 1563.5; DB 1; Length 461;
Best Local Similarity 64.9%; Pred. No. 4e-97;
Matches 294; Conservative 46; Mismatches 104; Indels 9; Gaps 4;

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QY 1 MGSTVPDLLPLVLELLVGYIGVPSYIGLVPHLCBDEKRDSCVPOCKYTHPONNSICTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGSTVPGLLPLVLRALVDVYPAGVHGLVHPGDRKREKESLCPOCKYSHPNRSICTT 60
QY 61 KCHKGYLYNDCEPGDGTCCRECEGSPFASENLHRLHSCSKCKREMGVEISSCTVD 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 KCHKGYLYNDCEPGDGTCCRECEGSPFASENLHRLHSCSKCKREMGVEISSCTVD 120
QY 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
QY 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 RDYVCGCRKNQRYHYWSENFQCFNCSLCNGVYHLSQOEKONTVCTCHAGFFLRENECV 180
QY 181 SCNSCKKSLSECTKICLPQIENWKTEDSGTTLVPLVIFPGCLLSLFTGLMRYGRWK 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 SCNSCKKSLSECTKICLPQIENWKTEDSGTTLVPLVIFPGCLLSLFTGLMRYGRWK 240
QY 241 SKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 SKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
QY 240 PKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 PKLYSIYCGSTPEKEGELGGTTKPLADNPSPPTGFTPLGSPVPSSTFTSSSTY 299
QY 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TPQDCPNF--AABREYAPPYOGADPILATALASDPINPDLQWEDSAHK---POSIDT 353
QY 354 DDPAATLYAVENVPLRMKEFVRRLGLSDHEIDRLQNGRCLEAOYSMLATWRRTPR 413
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 354 DDPAATLYAVENVPLRMKEFVRRLGLSDHEIDRLQNGRCLEAOYSMLATWRRTPR 413
QY 360 ADPAATLYAVVDGVPTRMKFEVRRLGLSEHEIERLELQNGRCLEAOYSMLAEWRRTRSR 419
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 ADPAATLYAVVDGVPTRMKFEVRRLGLSEHEIERLELQNGRCLEAOYSMLAEWRRTRSR 419
QY 413 REATLELGRVLRMDLGLCLEDIEEALCGPALPAPSLR 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 REATLELGRVLRMDLGLCLEDIEEALCGPALPAPSLR 452

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RESULT 4

GOMST1
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; I54537; I57826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:9187885; PMID:1849278
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <IEM>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <G62>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014; PMID:1647956
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lieslauer, W.
Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse "mf receptor type b.
A:Reference number: S19021; MUID:92039815; PMID:1657766
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Beck, B.F.

Query Match 62.9%; Score 1563.5; DB 1; Length 461;
Best Local Similarity 64.9%; Pred. No. 4e-97;
Matches 294; Conservative 46; Mismatches 104; Indels 9; Gaps 4;

Immunogenetics 39, 450-451, 1994
 A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1
 A:Reference number: 154532; MUID:94245292; PMID:8188324
 A:Accession: 154532
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-454 <RES>
 A:Cross-references: GB:L26349; NID:9430732; PIDN:AAA59361.1; PID:9430733
 R:Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steilmetz, M.
 Mol. Immunol. 30, 165-176, 1993
 A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
 A:Reference number: 157826; MUID:93156721; PMID:8381516
 A:Accession: 157826
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393, 'G', 395-454 <RE2>
 A:Cross-references: GB:M76656; NID:9202100; PIDN:AAA40465.1; PID:9202102
 C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (cd
 C:Genetics:
 A:Gene: TNFR-2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei
 F:1-29/Domains: signal sequence #status predicted <SIG>
 F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
 F:30-212/Domains: extracellular #status predicted <EXT>
 F:44-82/Domains: NGF receptor repeat homology <NG1>
 F:84-126/Domains: NGF receptor repeat homology <NG2>
 F:127-167/Domains: NGF receptor repeat homology <NG3>
 F:168-204/Domains: NGF receptor repeat homology <NG4>
 F:213-233/Domains: transmembrane #status predicted <MEM>
 F:236-454/Domains: intracellular #status predicted <INT>
 F:54,151,202/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 61.2%; Score 1521; DB 1; Length 454;
 Best Local Similarity 65.2%; Pred. No. 2,7e-94;
 Matches 294; Conservative 47; Mismatches 98; Indels 12; Gaps 7;

QY 1 MGISTVDDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCGKTIHQNNSTCCT 60
 DB 1 MGIPVPGILLVLLALMLGHPSCVLTGLVPSLGRKRDVSLCPGKTYVSHKNNISICCT 60
 QY 61 KCHKGTYLVNDGPGDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 DB 61 KCHKGTYLVNDGPGDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 QY 121 RDTVCGCRNQRHYWSENLFCFCNCLINGVHLSCOEKONTVCTCHAGFLRENECV 180
 DB 121 RDTVCGCRNQRHYWSENLFCFCNCLINGVHLSCOEKONTVCTCHAGFLRENECV 180
 QY 121 KDTVCGCRNQRHYWSENLFCFCNCLINGVHLSCOEKONTVCTCHAGFLRENECV 180
 DB 121 KDTVCGCRNQRHYWSENLFCFCNCLINGVHLSCOEKONTVCTCHAGFLRENECV 180
 QY 181 SCGNCKKSLKCTKLCI-POIENVKGTEDSGTIVLLPLVIFPGICLSLFLGIMRYORW 239
 DB 181 PSCHCKKNECKKLCIPLPLAVNTNPDGTAIVLLPLVILLCISLFFILCMCYPRW 240
 QY 240 KSKIVSYCGKSTPEKEGLESTTKPL--APNPSRSPRTGTPPLGFSFVSSSTFTSS 297
 DB 241 KREVSIICRDPVPVKE-EKAC--KPLTPAPSPAPSPSPSGNPTLGFSTGSPSSSVST 296
 QY 296 RYTPGDCP---NFAAPRRVAPRYOGADPILATATASDPILPDLQKWEBSAKRPOSITD 354
 DB 297 PLSPIFGPSNMHFMFVPSVSVPT-OGADPLALYESLCSVAPFSPVQKWEBSAH-PQRPDNA 354
 QY 355 DPATLYAVENVPLRKMEFVRRLGSLDHEIDRLQLONGRCRLREAOYSMLATWRRRTPRR 414
 DB 355 DPAITYAVVDGVPARWKEFMRFMGLSEHIERLEKONGRCRLREAOYSMLTAMRRRTPRH 414
 QY 415 EATLELGLVRLDMLGLEDIEEALGCPA 445
 DB 415 EDPLEVGLVLSKMLAGCLENILBALRNP 445

tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: 154182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
 A:Reference number: 154182; MUID:93252381; PMID:8486360
 A:Accession: 154182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762
 C:Genetics:
 A:Gene: LTBR
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.1%; Score 251.5; DB 2; Length 435;
 Best Local Similarity 29.7%; Pred. No. 1.5e-09;
 Matches 106; Conservative 33; Mismatches 133; Indels 85; Gaps 22;

QY 2 GLSTVDDLLPLVLELLVGIYPSGIVGLVPHLGDRKRDVCGKTIHQNNSTCCT 60
 DB 11 GLAMGP---LVIGLFGLLAASQPOAV---PYASENQTRDQ---EKEYEPOHR-ICCS 60
 QY 61 KCHKGTYLVNDGPGDPTDCRECSGFTASBNHRLHGLSCSKCKEMGOYEISCTVD 120
 DB 61 RCPRGTYVNAK-SRRTDVCAATCAENSTNEIMNYITLQCLRPDVPVGLIEIAPCTSK 119
 QY 121 RDTVCGCRNQRHYWSENLFCFCNCLINGVHLSCOE-KONTVCT-CHAGFL 174
 DB 120 RTOCRQCPGMCAWA---LECTHCELSDCPPEGAELKDEVGKGNHCVPKAGHF- 175
 QY 175 RNEECSCGNCKKSLKCTKLCI-POIENVKGTEDSGT-----VLL 214
 DB 176 -QNTSSPSARCPHRTCENOGL--VEADGTASDPTCKNPLEPPEPNSGTMMLAVLL 232
 QY 215 PLVIFGICLSLFLGIMRYORWKS-----KIVSYCGKSTPEKEGLESTTKPLA 268
 DB 233 PLAFPL---LNAVTFSCI-----KSHPSLCKRLGSL--KRRQGES----- 270
 QY 269 PNP---SESPTPG--FTPLGFSVPV-SSTFTSSSTYTPGDCPNRAAPRVAPRYQ 319
 DB 271 PNPVAGSWEPKRAHRYFPLDVLPLPISGDVSPVSGTLP-----AAYLEAGVPRQ 321

RESULT 6
 GGHUN
 nerve growth factor receptor precursor, low affinity [validated] - human
 N:Alternate names: NGF receptor
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1998 #sequence_revision 31-Mar-1998 #text_change 08-Dec-2000
 C:Accession: A25218; A60204; S21689; J57638
 R:Johnson, D.; Lanhahn, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bolhwell,
 Cell 47, 545-554, 1986
 A:Title: Expression and structure of the human NGF receptor.
 A:Reference number: A25218; MUID:87051725; PMID:3022937
 A:Accession: A25218
 A:Molecule type: mRNA
 A:Residues: 1-427 <JOH>
 A:Cross-references: GB:M14764; NID:9189204; PIDN:AA59544.1; PID:9189205
 R:Marano, N.; Dietzschold, B.; Farley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob,
 J. Neurochem. 48, 225-232, 1987
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth fa
 A:Reference number: A60204; MUID:87085574; PMID:3023363
 A:Accession: A60204
 A:Molecule type: protein
 A:Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56 <MAR>
 A:Experimental source: melanoma cell line A875
 A:Note: this sequence has been corrected by a note added in proof to follow the nucle
 R:Visavajjala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.


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Db      246 RGTITD-----LITVYCSIIAAVVGGLVATIAFRKRWNSCKONKOGANSRPVNGT----- 294
OY      332 DPIDNPLQKWEDESAHKPOSILDTDDPAT-----LYAVV-----ENVEPL-- 369
Db      295 -PPEBGEKHLSDGSIWSDGSLHDQTHQTFAGQALKGKGNLYSLPLTKREVEKELN 353
OY      370 --RWKEFVRRLGLSDHEIDRLQLQNGRCLEAOYSMLATWRRPTPREATLELGLVLRD 427
Db      354 GDTWRIAGLELGYOPEHID--SFTHEACPEYRA--LLASWAGD---SATLIDALLAALRR 405
OY      428 MDLLGCLDEIEALC 442
Db      406 IQ-----RADIVESLC 416

RESULT 8
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634; A40254; S54816
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A:Reference number: A38634; MUID:91187885; PMID:1849278
A:Accession: B38634
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <LEM>
A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A:Reference number: A40254; MUID:91246168; PMID:1645445
A:Accession: A40254
A:Molecule type: mRNA
A:Residues: 1-474 <GOO>
A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828
R:Kisomerneghs, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
A:Reference number: S54816
A:Accession: S54816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <RIS>
A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C:Keywords: cytokine receptor; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F:40-77/Domain: NGF receptor repeat homology <NG1>
F:79-120/Domain: NGF receptor repeat homology <NG2>
F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match      8.2%; Score 205; DB 2; Length 474;
Best Local Similarity 26.4%; Pred. No. 2.1e-06;
Matches 67; Conservative 30; Mismatches 105; Indels 52; Gaps 11;

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Db      213 PRTLYV-----SDEP-----TRSQPLDQSPGS 236
OY      275 PTPGFTPLGFSPEV 288
Db      237 QPFSILSLSGSPFI 250

RESULT 9
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I48854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: I48854; MUID:95178848; PMID:7873884
A:Accession: I48854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:9433831
C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match      8.2%; Score 204.5; DB 2; Length 459;
Best Local Similarity 23.7%; Pred. No. 2.2e-06;
Matches 83; Conservative 43; Mismatches 145; Indels 79; Gaps 15;

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OY      44 CPQGKTIHPQNNISICTKHKGTLYLNDPFGQDPTDCRECSGFTASENHLRLCLSC- 102
Db      40 CQISQETRYRKAKMCCAKPRQGYVKNFC-NKTSPTVCADCCASMTQYWNQFRCLSCS 98
OY      103 SKCRKEMGOVEISSCTVDHDTVCGCRKNQY----RHYMSENLFQCFNCSLCLNG-TVHLS 157
Db      99 SSGCTID--QVEIRACTKQONRVACACAGRYCALKTH--SGSQRQCMRLSKCGPGGVAS 154
OY      158 COEKONTVC-TCHAGFPLENEVCSCNCKSLLECTKLCPLPIENVKG--TEDSGTIVLL 214
Db      155 RAPNGNVLCKACAPGTF--SDTTSSTDYCRPHRISIIAIPGNASTDAVCAPESTLSAI 212
OY      215 PLVIFPGICLLSLPLIGLWRYQRMKSKLYSVCGKSPPEKGELEGTTTKLAPNPSPS 274
Db      216 PRTLYV-----SDEP-----TRSQPLDQSPGS 236
OY      275 PTPGFTPLGFSPEV 288
Db      237 QPFSILSLSGSPFI 250

RESULT 10
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C:Species: myxoma virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: A40566
R:Ruppon, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A:Reference number: A40566; MUID:91335768; PMID:1651597
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPN>
A:Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-117/Domain: NGF receptor repeat homology <NG3>
F:166,181,205,238/Binding site: carboxylate (Asn) #status predicted

```


Query Match 8.0%; Score 200; DB 1; Length 326;
Best Local Similarity 25.8%; Pred. No. 3.1e-06;
Matches 62; Conservative 28; Mismatches 88; Indels 62; Gaps 10;

QY 14 LVLLELVGIPSGVIGLPHLSDREKRDVCPGKTIHPONNSICCKKHKGTLYNDP 73
DB 6 LLLAVYACVGGG---APIGADGK---CRGNDY---EKDGJCTCTCPPGSAYSLIC- 53
QY 74 GPCODTDCRECSGSPFASSENHLRHCLSC-SKCRKMGQVEISCTVDRTVCGCRKNQY 132
DB 54 GPGSDTYCSPCKNETFASNNHAPACVSCRGCTGHLs--ESQCDKTRDYCDCAAGNY 111
QY 133 -----RHYSNLFQCFNCSLCLNG- 152
DB 112 CLKKGQCRICAPKTKCPAGYGVSGHTRTGDVLCCTKCPRTYSDAVSTETCTSSFNVI 171
QY 153 TVHLSCQEKONTVCTCHAGFLRENECVSCSNCKSL---ECRCLCLPQJENKVGTEDSG 209
DB 172 SVENFLYPVNDTCTTAG---PNEVYKTSSESVTLNHTDCDPVHTETTYGTSSEGAG 227

RESULT 11
JN0006
nerv growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reich
Neuron 2, 1133-1134, 1989
A>Title: Structure and developmental expression of the nerve growth factor receptor in t
A:Reference number: JN0006; PMID:90166579; PMID:2560385
A:Accession: JN0006
A:Molecule type: mRNA
A:Residues: 1-416 <LNR>
A:Experimental source: embryonic chick brain
R:Heuer, J.G.; Faltmele-Maiale, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A>Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; PMID:90152140; PMID:2154393
A:Accession: A60504
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 21-35, 'V', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
F:1-20/DNA: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <EXT>
F:21-219/DNA: extracellular #status predicted <EXT>
F:24-57/DNA: NGF receptor repeat homology <NG3>
F:59-100/DNA: NGF receptor repeat homology <NG2>
F:101-139/DNA: NGF receptor repeat homology <NG3>
F:141-181/DNA: NGF receptor repeat homology <NG4>
F:189-237/Region: serine/threonine-rich
F:240-261/DNA: transmembrane #status predicted <MEM>
F:262-416/DNA: intracellular #status predicted <INT>
F:2/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9%; Score 196.5; DB 1; Length 416;
Best Local Similarity 22.8%; Pred. No. 6.9e-06;
Matches 114; Conservative 63; Mismatches 155; Indels 169; Gaps 32;

QY 11 LPLVLELLVGIYPSGIVGLPHLSDREKRDVCPGKTIHPONNSICCKKHKGTLYN 70
DB 5 VPLLL-----LIPAG-----PTWGSKEK-----CLTKMY---TTSGCCACACNIGEGVQ 47
QY 71 DCPGCDTDCRECSGSPFASSENHLRHCLSCSKCRKMGQVEIS-CTVDRTVCGCR 128
DB 48 PC-GVNO-TYCEPCLDSVTYSDTYSATPECKPCTQC---VGLHSMAPCVESDADVRC- 101

QY 129 KNOYRHWSENLFQCFNCSLCLNG-TVHLSCQEKONTVC-TCHAGFLRE---NECVSC 182
DB 102 --AVGYFODELSGCKSCSCICEVGFGLMPCRDSDTYCEBCEPGTSDANFVDPCLPC 159
QY 183 SNCKSLSECLKCLCPQJENKVGTEDSGTLYNLFVIFGCLSLSLTGLMRYQRKSK 242
DB 160 TICEENVMVKEC-----TATSDACRDLHP----- 190
QY 243 LVSIVCSKSTPEKEGELEGTTRPLAPNPSFPTPGTPIAGSPVPSSTFTSSSTTPG 302
DB 191 TPST-AGSDPE-----PITRDP--FN-TEGATTLA-DIYTWAGSSGPVYSRG 235
QY 303 DCPNFAAPRREAVPY-----OGAD--PILATALASDP 333
DB 236 TADN-----LIPVCSILAAVVGVLVAYIAFRMNSCKQKQANRRVNGT-----P 283
QY 334 IPNPLQKWESA-----HKPQSLDDPDA-----TLXAVENVPLR----- 370
DB 284 SPEGEKLHSDSGISVDSQSLHDQPPNOSTQGPAPKDGSLYA--SLPSSKEVEYKEL 340
QY 371 -----WKEFVRRLGSDHEIDRLFLONGRCLEAQA---YSMLATWRRRRPREATTLEL 420
DB 341 SSNAETWRLQAGELGKEDLID-----CTRESPARALLADN---SAKETATLDA 389
QY 421 LGRVLRMDLGLCLEDIEAL 441
DB 390 LVLALRKIQ---RGDIAESL 406

RESULT 12
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Opton, C.; Delange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A>Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
A:Reference number: A43692; PMID:87321103; PMID:280128
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:64-105/DNA: NGF receptor repeat homology <NG3>
F:106-147/DNA: NGF receptor repeat homology <NG3>

Query Match 7.7%; Score 192; DB 2; Length 325;
Best Local Similarity 24.7%; Pred. No. 1.1e-05;
Matches 73; Conservative 34; Mismatches 108; Indels 80; Gaps 14;

QY 9 LPLVLELLVGIYPSGIVGLPHLSDREKRDVCPGKTIHPONNSICCKKHKGTLY 68
DB 1 MLRLIALLVGVVYVYGD---VPYSSNGK---CGGHDY---EKDGLCCASCHPGFYA 49
QY 69 YNDPCGODTDCRECSGSPFASSENHLRHCLSC-SKCRKMGQVEISCTVDRTVCGCG 127
DB 50 SRLC-GGGSNTVCGPCEDGFTTASTNHPACVSCRGCTGHLs--ESQCDKTRDYCDCA 106
QY 128 RKNQYRHWSENLFQCFNCSLCLNGTVHLSCQEKONTVCTCHAGFLRENECVSCSNCKR 187
DB 107 STGNVCLLKQCN-----GCRICAPQ-----KCPAGYGVSGHTRAADTLCCK 148
QY 188 SLECTKICLPQI--ENKRGEDSGTIVLPLVIFGCLSLSLTGLMRYQRKSKLYS 245
DB 149 -----CPHTYSDSLSPETGCTG-----FNISVGFNLXP 179
QY 246 IVCSKSTPEKEGELEGTTRPLAPNPSFPTPGTPIAGS---VPSSPTSSS 297
DB 180 V-----NEISCTT---AGHNEVIKTKETTYTLANTDQDPVHTETTYANS 221

A:Molecule type: mRNA
 A:Residues: 1461 <END>
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.R.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Dombic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690; PMID:196549
 A:Accession: A48416
 A>Status: preliminary
 A:Molecule type: mRNA, protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA819824.1; PID:g235649
 A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AA63262.1; PID:g339752
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors
 A:Accession: A23666; MUID:91056048; PMID:2173696
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40/65-69; 136-141; 300-306 <LOB>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for a reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: B35010
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kühnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 A:Gene: GDB:TNFR2
 A:Accession: I36.2-1p36.2
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: the 1st of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.4%; Score 183.5; DB 1; Length 461;
 Best Local Similarity 24.9%; Pred. No. 5,7e-05;
 Matches 72; Conservative 29; Mismatches 103; Indels 85; Gaps 14;
 QY 42 SYCPQCKYIHPONNSICCTCHNCTLYLNCPGCGOTDRECSGSFTASENHLRCLS 101
 DB 38 STCRRLREY-IDQTAQWCCSKSCSPQAHAKVFCT-KTSPTVCDCSDSTYTQIMNVPCLLS 95
 QY 102 C-SKREKMGQVEISCTVDRTVCGCRKNQRYHMSENLFOCPNCSICLNGVHLSQOE 160
 DB 96 CGSRCSDD--QVETQACTRQNRICTCRPG-----WICALSKQSCRLCA----- 138
 QY 161 KQNTVCTCHAGFFL-----RENECVSCSNC-----KSLSECTKLCLP-QIENVKCTEDSGT 210
 DB 139 ---PLRRCRPGFVGVARBGTETSDVVCXPCAPGTFSTNTSTSDICRPHQICNV----- 187
 QY 211 TVLLPLVIFPGCLLSLFLIGLMRYORWMSKLSYICGASTPEKEBELGCTTKPLAPN 270
 DB 188 -VALP-----GNASMDAVCTSTSP-----TRSNAPG 212
 QY 271 PSFSPTPGFTPTLGFSVPVS-STFTSSSTYP-----GDCPNFAAP 310
 DB 213 AVHLPOVSTRSQHTQPTPERSTAPSTSLPLPKPSPPAEGSTGDFALP 261

Search completed: December 27, 2002, 15:08:18
 Job time : 23 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 27, 2002, 15:07:00 ; Search time 36 Seconds
(without alignments)
2604.207 Million cell updates/sec

Title: US-09-899-429a-2

Perfect score: 2487
Sequence: 1 MGLSTVPDLLPLVLLELV.....DIEBALGPALPPAPSLR 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL.21:*
2: SP_Bacteria:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriap:*
17: SP_Archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1801.5	72.4	446	6 Q95ND3	Q95ND3 felis silve
2	873	35.1	189	6 Q97530	Q97530 canis fami
3	866	34.8	189	6 Q95185	Q95185 felis silve
4	381.5	15.3	413	11 Q99MM1	Q99MM1 mus musculu
5	331	13.3	387	11 Q8VD70	Q8VD70 xenopus lae
6	233	9.4	387	11 Q9PVD4	Q9PVD4 xenopus lae
7	230.5	9.3	433	11 Q912M6	Q912M6 rattus norv
8	227.5	9.1	368	13 Q57408	Q57408 melagris g
9	225	9.0	438	13 Q9DFV0	Q9DFV0 brachydanio
10	211	8.5	357	13 Q9DF34	Q9DF34 brachydanio
11	204.5	8.2	459	11 Q62327	Q62327 mus musculu
12	203.5	8.2	482	11 Q88734	Q88734 mus musculu
13	197	7.9	368	13 Q91AR7	Q91AR7 gallus gall
14	189.5	7.6	320	6 Q9XS29	Q9XS29 oryctolagus
15	189	7.6	319	6 Q9TV79	Q9TV79 oryctolagus
16	189	7.6	333	6 Q9BDP2	Q9BDP2 macaca mula

17	188	7.6	302	13 Q9PUS0	Q9PUS0 salveinus
18	188	7.6	331	6 Q9BDN0	Q9BDN0 macaca neme
19	187.5	7.5	334	6 Q9GL40	Q9GL40 macaca mula
20	187.5	7.5	651	13 Q98SM6	Q98SM6 gallus gall
21	187	7.5	368	13 Q9PW79	Q9PW79 gallus gall
22	186	7.5	331	6 Q9TSM4	Q9TSM4 macaca fasc
23	185.5	7.5	328	6 Q9BDP0	Q9BDP0 actus trivi
24	184	7.4	331	6 Q9BDA4	Q9BDA4 cercocebus
25	183.5	7.4	331	6 Q9BDA4	Q9BDA4 cercocebus
26	182.5	7.3	285	13 Q9DGH7	Q9DGH7 gallus gall
27	179	7.2	320	12 Q57079	Q57079 cowpox viru
28	179	7.2	322	12 Q72761	Q72761 cowpox viru
29	176.5	7.1	327	6 Q97491	Q97491 ovis aries
30	176	7.1	257	6 Q97491	Q97491 ovis aries
31	176	7.1	277	6 Q8WMQ2	Q8WMQ2 ovis aries
32	176	7.1	283	6 Q9XS28	Q9XS28 cercocebus
33	175.5	7.1	312	13 Q9DGH8	Q9DGH8 cercocebus
34	174.5	7.0	320	12 Q57091	Q57091 ectromelia
35	174.5	7.0	320	12 Q57300	Q57300 ectromelia
36	174.5	7.0	347	12 Q57119	Q57119 ectromelia
37	174	7.0	347	12 Q57115	Q57115 cowpox viru
38	174	7.0	350	12 Q57123	Q57123 cowpox viru
39	174	7.0	351	12 Q57121	Q57121 cowpox viru
40	173	7.0	401	13 Q9PBG7	Q9PBG7 xenopus lae
41	172.5	6.9	349	12 Q57100	Q57100 monkeypox v
42	172.5	6.9	350	12 Q57118	Q57118 cowpox viru
43	171.5	6.9	316	12 Q57092	Q57092 ectromelia
44	171.5	6.9	348	12 Q57277	Q57277 monkeypox v
45	171	6.9	326	12 Q57120	Q57120 cowpox viru

ALIGNMENTS

RESULT 1

ID: Q95ND3 PRELIMINARY; PRT: 446 AA.
AC Q95ND3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR I.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB051103; BAB5455.1; -;
DR InterPro: IPR000345; CYTC_heme_bld.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS0116; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 72.4% Score 1801.5; DB 6; Length 446;
Best Local Similarity 75.8%; Pred. No. 1.1e-150;
Matches 348; Conservative 28; Mismatches 66; Indels 17; Gaps 8;

```

QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLGDREKRDVSCPGKXIHPQNNISICT 60
DB 1 MGLPTVPGLLQPLVLLALVETPLRVTGLVPLRDREKRALPCPGKXIHPQNNISICT 60
QY 61 KCHKGTLYLNDPCPGPQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
DB 61 KCHKGTLYLNDPCGPGDPTDRCRENGTFTASENHLRHCLSCSKCKRMKGVEISSCTY 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKSLKCTKICLPQLENNKGFEDSGTIVLLPVTFEGCLISLTLGLMYRQRRK 240
DB 181 SCVNCCKNTECKTCLPVEIVKDPDPTVLLPVTFEGCLISLTLGLMYRQRRK 239
QY 241 SKLSTVSCSKSTPEKGELEGTTPKPLAPNPSFPTPGTTLGFSVPSTFTSSTYT 300
DB 240 SKLSTVSCSKSTPEKGELEGTTPKPLAPNPSFPTPGTTLGFSVPSTFTSSTYT 288
QY 301 PDDCPNF--AABREYAPPYQADPILATVALASDPIPNFLQKWECSAH--KQSLDTDDP 356
DB 289 PSDMANLRAASYSREKAPPYQAGPILSAPASSPSTPYQKWECSHTHQREDA--DPADP 347
QY 357 ATLTVAVVENVPPLRKKEFYRRLGSDHETDRLQNGRCLRAQYSMLATWRRRTPRRA 416
DB 348 ATLTVAVVENVPPLRKKEFYRRLGSDHETDRLQNGRCLRAQYSMLATWRRRTPRRA 407
QY 417 TELLAGRVLRMDLLGLCEDEIEALCGPAPLPPAPSLR 455
DB 408 TELLAGRVLRMDLLGLCEDEIEALCAPASLSAPRLLR 446

```

RESULT 2

```

ID 097530 PRELIMINARY: PRT: 189 AA.
AC 097530:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21109092; PubMed=11182158;
RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Dutchie S.,
RA Bennett D.;
RT "Cloning of canine IL-1ra, TNFR and TIMP-2.";
RL Vet. Immunol. Immunopathol. 78:207-214 (2001).
DR EMBL; AF013955; AAD01516.1; -.
DR HSSP; P19438; 1TEXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21324 MM; 5D3AD6A5676BE99 CRC64;

```

Query Match

Best Local Similarity 35.1%; Score 873; DB 6; Length 189;
Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

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QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLGDREKRDVSCPGKXIHPQNNISICT 60
DB 1 MGLPTVPGLLQPLVLLALVETPLRVTGLVPLRDREKRALPCPGKXIHPQNNISICT 60

```

```

QY 61 KCHKGTLYLNDPCPGPQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
DB 61 KCHKGTLYLNDPCGPGDPTDRCRENGTFTASENHLRHCLSCSKCKRMKGVEISSCTY 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKS 188
DB 181 SCVNCCKN 188

```

RESULT 3

```

ID 095185 PRELIMINARY: PRT: 189 AA.
AC 095185:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor p60 (Fragment).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Dutchie S., Nasir L., Eckersall P.D.;
RT "Felis catus tumor necrosis factor receptor p60 (TNFR-1) mRNA,
RT partial cds.";
RL Submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1TEXT.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MM; F3FBE0CE809D7DBE CRC64;

```

Query Match

Best Local Similarity 34.8%; Score 866; DB 6; Length 189;
Matches 155; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

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QY 1 MGLSTVPDLLPLVLLLELVGTPSGVIGLVPHLGDREKRDVSCPGKXIHPQNNISICT 60
DB 1 MGLPTVPGLLQPLVLLALVETPLRVTGLVPLRDREKRALPCPGKXIHPQNNISICT 60
QY 61 KCHKGTLYLNDPCPGPQDTCRECSGSFTASENHLRHCLSCSKCKRMKGVEISSCTVD 120
DB 61 KCHKGTLYLNDPCGPGDPTDRCRENGTFTASENHLRHCLSCSKCKRMKGVEISSCTY 120
QY 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
DB 121 RDTVCCGRKNQRYHYWSENLFOCFNCSLCINGVHLSCEBKONTVCTCHAGFFLRNECV 180
QY 181 SCNCKKS 188
DB 181 SCVNCCKN 188

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RESULT 4

Best Local Similarity 35.1%; Score 873; DB 6; Length 189;
Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

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ID 099MM1 PRELIMINARY: PRT: 413 AA.
AC 099MM1:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

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DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE WSL-1-like protein.
 GN TNFRSF12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA MEDLINE=21158384; PubMed=11261933;
 RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
 RT Owen M.J.,
 RT "Genomic structure, expression, and chromosome mapping of the mouse
 RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
 RT gene."
 RL Immunogenetics 53:59-63(2001).
 DR EMBL: AF329969; AAK11256.1; -.
 DR HSSP: P25943; 1CDP.
 DR MGD: MGI:1934667; Tnftrsf12.
 DR Interpro: IPR000488; Death.
 DR Interpro: IPR000561; EGF-like.
 DR Interpro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85DDABAF CRC64;

Query Match 15.3%; Score 381.5; DB 11; Length 413;
 Best Local Similarity 30.1%; Pred. No. 2, 2e-25;
 Matches 139; Conservative 53; Mismatches 176; Indels 91; Gaps 23;

QY 9 LLEPLVLELLVGIYPSGVTGLVPHLDREKDSVCPQGIYINPONSICCTCKHKT 68
 DB 18 LLLLLLLLLLLGGGOGGMSGRCDASESQK-----YGPCCRCGPKGHY 64
 QY 69 YNDCPGPGDTRCCEGSGFTASENHLR-HCLSCSKCKEMGOYEISCTVDRTYVC 127
 DB 65 KAPAEPCGNSCTCLPCPSDFLTFRDNHFKTDCTRCQVCDERALQVTLNCSAKSDTHCGC 124
 QY 128 RKNQRYHWSNLEFCQNCISCLING-TVHLSG-----QEKONTVCTCHAGFLENE 178
 DB 125 QSG-----W-----CVDCSTVPCGKSPSCVPCGATTPVHEAPTRPRCLPGFYINGND 173
 QY 179 CVSC-----SNCKSLSECTKLCPLQIENVKGTEDS-GTVVLLPLVIFFGCLLSLFLIGL 232
 DB 174 CTSCPTGTFSSVCPKA--CTAVC-----GKMFVQVLLGVAFLEGAILLIC----- 217
 QY 233 MYRQHKSKSYISVCGKSPKEGELEGTTRKPLA-PNPSFPTPGFTPLTIGSPVSS 291
 DB 218 --AICRQD-PCKAVV---TADTAG-----TEPLASQTAHLASASASAPL-LAP-PS 262
 QY 292 TTFSSST-----YTPGDCPNFAAPREVAAPY-QGADPLATALASDPIPNLQWED 343
 DB 263 TGKICTTIVQVGNWPTGLSOTGEVCGQASQPMDOPLNRTLGTPPLASPLSPAP----- 316
 QY 344 SAHKPSGLDIDPATLYAVENVNPLRMKEFVRRLGSDHEIDRLQNGRCLEADQYSM 403
 DB 317 PAFSPAIVLPGP-QLYDVMDAVPARMKKEFVRTLGREAIEAIVEICR-FRDOQYEM 374
 QY 404 LATWRRTPRREATLELLGRVLRMDLGLCLEDIEAL 441
 DB 375 LKRRQDP---AGLCAIYAALERKGLBGCAEDLRSL 409

RESULT 5
 Q9VD70 PRELIMINARY; PRT; 387 AA.
 ID Q9VD70

AC Q9VD70;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 12.
 GN TNFRSF12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SALIVARY GLAND;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC017526; AAI17526.1; -.
 DR MGD: MGI:1934667; Tnftrsf12.
 DR Interpro: IPR000488; Death.
 DR Interpro: IPR000561; EGF-like.
 DR Interpro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KM Receptor.
 SQ SEQUENCE 387 AA; 41640 MW; F1664466BAD68D3 CRC64;

Query Match 13.3%; Score 331; DB 11; Length 387;
 Best Local Similarity 27.9%; Pred. No. 5, 8e-21;
 Matches 127; Conservative 50; Mismatches 158; Indels 120; Gaps 21;

QY 9 LLEPLVLELLV--GIYPSYTGIVPHLDREKDSVCPQGIYINPONSICCTCKHKT 66
 DB 27 LLEPLVLELLVLLGGGOGGMSGRCDASESQK-----YGPCCRCGPKGH 73
 QY 67 YLYNDCPGPGDTRCCEGSGFTASENHLR-HCLSCSKCKEMGOYEISCTVDRTYVC 125
 DB 74 YMKAPCAEPCGNSCTCLPCPSDFLTFRDNHFKTDCTRCQVCDERALQVTLNCSAKSDTHC 133
 QY 126 GCRKNQRYHWSNLEFCQNCISCLINGTVHLSGQEKONTVCTCHAGFLENECVSCSN 184
 DB 134 CGQSG---W-----CVDCSTE 146
 QY 185 -CKSLSECTKLCPLQIENVKGTEDSGTVLL---PLVIFGCLLSLFLIG---LMTRYQ 237
 DB 147 PCGKSSPFS--CVP-----CGATTPVHEAPTRPLFWQVLLGVAFLEGAILICAYC 194
 QY 238 RW---KSKIVSYCGKSTPEKEGELEGTTRKPLAPNPSFPTPGFTPLTIGSPVSSFT 294
 DB 195 RMQCKAVVADTAGTET-----LASPQTAHLASAS-----ATL-LAP-PSSTGK 239
 QY 295 SSSST-----YTPGDCPNFAAPREVAAPY-QGADPLATALASDPIPNLQWEDSAH 346
 DB 240 ICTTIVQVGNWPTGLSOTGEVCGQASQPMDOPLNRTLGTPPLASPLSPAP-----PAG 293
 QY 347 KPSGLDIDPATLYAVENVNPLRMKEFVRRLGSDHEIDRLQNGRCLEADQYSMLAT 406
 DB 294 SPAIVLPGP-QLYDVMDAVPARMKKEFVRTLGREAIEAIVEICR-FRDOQYEMLR 351
 QY 407 WRRTPRREATLELLGRVLRMDLGLCLEDIEAL 441
 DB 352 WRQDP---AGLCAIYAALERKGLBGCAEDLRSL 383

RESULT 6
 Q9PVD4
 ID Q9PVD4 PRELIMINARY; PRT; 387 AA.
 AC Q9PVD4
 DT 01-MAY-2000 (Tremblrel. 13, Created)

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DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE P75-1-like transmembrane protein fullback.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RX [1]
RN SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
RT Expressed Xenopus Gene.";
RT Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AF131890; AAD34072.1; -.
DR HSSP; P07174; INGR.
DR InterPro: IPR001083; Copper_f1st.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART; SM00412; Cu_F1ST; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
KW transmembrane.
SQ
SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

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Query Match          9.4%; Score 233; DB 13; Length 387;
Best Local Similarity 22.6%; Pred. No. 2.6e-12;
Matches 105; Conservative 63; Mismatches 166; Indels 130; Gaps 25;

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QY 12 PVLLELVGIYPSGVIGLVPHLGREKRDVSCPOGKTIHPONNSICTCKCHKGTLYND 71
DB 6 PVLTLCLL-----LISKISADYCESGLY--TNSKCCSLCPAGFCVVP 49
QY 72 CGPGQDPTCCREC-ESGFTASENHLRHCLSCSKCKEMGOVEISCTYDRDTCGRKN 130
DB 50 C--GSDTCEPCIENSTPSDVSAKAKQCPCTCSPSLTLE-SNCTREODPTVCRCPER 106
QY 131 QYRWYSEMLFOCFNCSLCLNG-TVHLSCQEKONTVC-TCHAGFLR---ENECVSC-S 183
DB 107 QULD--SNK--CLPCQLCSKHGVYSQCTHNKNYQCQLCSSGFYSEVSSSPCLPCT 162
QY 184 NCKSELECTKLCLEPOLEENKGTEDSGTYLPLVIFGLCLSLFLGIMRYORKSKL 243
DB 163 ECKEFVQIGDCVPO----- 177
QY 244 YSLVC-GKSTP---EKEGLEGTTRKPLAPNPSFSP---TPGFTPLLGSPVPSSTFTSS 296
DB 178 HDILCDKDVPLIKRTGEGENGT---AGSPHFIPODNSKNIPV--YCSIIAAVVGVL 231
QY 297 STYTPGDCNPFAPRREVAPRYOGADPILATFALASDPINPQKWD--SAHKPOSIDTD 354
DB 232 IAYVAFKCTTCKOKKQAKARAGE---LATSTEGEKLINDSGVFIDTSLDPEPHLSK- 287
QY 355 DPATLYAVE-----NVPLR-----WKEFYRRGLSDHEIDRLQLONG 393
DB 288 -----AKTEPKLYINLPHKQSEVERLADTSLGDMQRLASLGLYEETIDTF-----G 337
QY 394 RLREKQVSMATWRRRTTRREATTELLGRVLRDMDLGLCEDDI 437
DB 338 RG-EDPVHLLTDW---SSKESSTLEVLCALVNMERADYVENTL 377

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RESULT 7
ID 0912M6 PRELIMINARY; PRT; 433 AA.
AC 0912M6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)

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DT 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE Tumor necrosis factor receptor type II (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Osburn B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AF420214; AAL16021.1; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
FT NON_TER
FT NON_TER
SQ
SEQUENCE 433 AA; 45723 MW; 7573D835E72CA4A CRC64;

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Query Match          9.3%; Score 230.5; DB 11; Length 433;
Best Local Similarity 24.7%; Pred. No. 4.9e-12;
Matches 91; Conservative 46; Mismatches 152; Indels 79; Gaps 16;

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QY 24 PSGVIGLVPHLDREKRDVSCPOGKTIHPONNSICTCKCHKGTLYNDGPGQDPCRE 83
DB 4 PAKYV-LTRY---KRPNGQCISQEIYDKKAMCCAKPPGOYAKHFC-NKTSPTVCAD 58
QY 84 CEGSFTASENHLRHCLSC-SKCRKEMGOVEISCTYDRDTCGRKNQY--RHWSENL 140
DB 59 CAAGMTQYWNHLHCLSCSSSSCSDD--QVETHNCTKNQRYCACNADSYCALKLSGNC 116
QY 141 POCFNCSLCLNG-TVHLSCQEKONTVC-TCHAGFLREBVCSCNCKSLCTKLCPL- 197
DB 117 RCKMKLSKGPFGVARSHTSNGNVCISACAPGT--STTSSTVDCRPHRCSILATPG 174
QY 198 -----QIENVGTGDS-----GTT----- 211
DB 175 NASTDAVCASESPTPSAVPRITIVSOPETRSQPMQDQEPGQTHIPVSLSTPIERS 234
QY 212 ----VLPLVIFGGLCLSLFLGLMYRYORKSKSIYVCSKSPKEGELEGTTRKPL 267
DB 235 ITGGISLPIGLIVGLTTLGLMLGL-----ANCFILYQKKRPPSC--LQRETMVPH 283
QY 268 APNPSPPTPGTTPILGSPVPSSTFTS-SSTYTGCD--CPNFAAPRRVAPPYGADPI 324
DB 284 LPDEKSDQAVGLEQHLITLTAAPSSSSSSLESSASAGDRRAPGVIPQARVTAEOGSOEA 343
QY 325 LATALASD 332
DB 344 CAGSRSSD 351

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RESULT 8
ID 057408 PRELIMINARY; PRT; 368 AA.
AC 057408;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Subgroup E AIV receptor.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OC NCBI_TaxID=9103;
RX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97471016; PubMed=9326659;
RA Adkins H.B., Brojatsch J., Naughton J., Rolis M.M., Resola J.M.,

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RA Young J.A.:
 RT *Identification of a cellular receptor for subgroup E avian leukosis
 RL virus.";
 DR Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).
 DR EMBL: AF060002; AB93987.1; -
 DR HSSP: 014763; 1D0G.
 DR InterPro: IPR001450; 4Fe4S_ferredoxin.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001865; Ribosomal_S2.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000531; death; 1.
 DR Pfam: PF000020; TNFR_c6; 2.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 368 AA; 41020 MW; 5701AC2A6DAF87E2 CRC64;
 Query Match 9.1%; Score 227.5; DB 13; Length 368;
 Best Local Similarity 23.8%; Pred. No. 7.4e-12;
 Matches 107; Conservative 46; Mismatches 172; Indels 125; Gaps 19;
 QY 14 VLLELVGIVPSGVIGLVPHLGDEKRDVSCPGQKVIHPONNSICTCHKGTLYNDGP 73
 DB 11 VLLLLALKV-----HLGSAAVAKRAVKSVDLKPDPYS--KKCPKGTLYAND-- 55
 QY 74 GPGDDTCRCESGFTASENHLRHCLSCSKCKEMGOVEISSCTVDRDYVCGCRKNQYR 133
 DB 56 ----SSKCLPKCKDEYETPRDPKCLGCRTRCD--QVEVSPCNSTRNTRCACK----- 104
 QY 134 HYWSENFQCFNCSLCINGVHLSGOEKONTVCTCHAGFLRENECVSCSNCK----- 186
 DB 105 -----NGT-----FCLPDHPCEMCKCKQCRKPCQ 129
 QY 187 -KSLCTK---LCLEPQIENVKGTEDSGTV--LLPLVIFEGCLLSLFT-----G 231
 DB 130 VIRACQOQSDLRGCPPLDSSSFTTGIISTVLPVLLVLLVLLCCCCRRYSAGSG 189
 QY 232 LMYVQRMKSLYSIVCGKSPKEKEGEGTTTKPLAPNPSFSPPTPTLIGTSPVSS 291
 DB 190 VLSSKPRAMKILL-----QRMGIQDNQNCNQITVQOQOQOQOQLITTEQG--SEVPRG 240
 QY 292 TETSSYTPGDCPNFAAPRREVAPPYOGADPILATALASDPINPLOKMEDSAHKPQSL 351
 DB 241 VEVEVEEVAR--RTPNVETQRLV--PYPGKDP--TVLSS-----SF 277
 QY 352 DTDDPATLYAVENVPLRMKEFVRLGLSDHEIDRLONGRCLEAQAQSMLATWRRT 411
 DB 278 NT-----FVDLVPQMRFRGALGLRENNLYQAE-QNDRSGEPLYMLIMLMKE 328
 QY 412 PRREATLELGRVLRMDLGLCLEDIEAL 441
 DB 329 GSK-ASVNTLETLSQISLGSVADIASEL 357
 RESULT 9
 Q9DFV0 PRELIMINARY; PRT; 438 AA.
 AC Q9DFV0;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Ovarian TNF receptor.
 CN TNFRSF1A.
 OS Brachydanio rerio (Zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J., Goetz F.W.;
 RT "Molecular cloning and expression of a TNF receptor and two TNF
 RT ligands in the fish ovary."
 RL EMBL: AF250042; MAG24365.1; -
 DR HSSP: 014763; 1D0G.
 DR ZFIN: ZDB-GENE-010802-1; tnfrsf1a.
 DR InterPro: IPR000345; Cyt_c_heme_bld.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000531; death; 1.
 DR Pfam: PF000020; TNFR_c6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;
 Query Match 9.0%; Score 225; DB 13; Length 438;
 Best Local Similarity 21.7%; Pred. No. 1.5e-11;
 Matches 111; Conservative 53; Mismatches 170; Indels 178; Gaps 24;
 QY 1 MGLSTVPDLLPLVLELVGIVPSGVIGLVPHLGDEKRDVSCPGQ-KYIHPONNSICG 59
 DB 1 MDKSEAMKVCMAVIFSLALVGHGAELGVSADQNTARMTLENHETP---NPFCC 57
 QY 60 TKCHKGTLYLNDGCPGPDYDTCRCESGFTASENHLRHCLSCSKCKEMGOVEISSCTV 119
 DB 58 KNCAGETVYKEKTSQGVHMGKSPCEKGTVAEHTGTGHEOCICQCHRDQ----- 107
 QY 120 DQTVCGCRKNQYRHYWSENFQCFNCSLCINGVHLSGOEKONTVCTCHAGFLRENE- 178
 DB 108 -----TVVABCTYSTMTKCDCKFGTCLDDEP 134
 QY 179 ---CVSCSNCKKSLCTKCLP-----QLENVGTEDESGTT-VLLPLVI 218
 DB 135 CEVCKKCTCKCADEEYSGCPTSNTRKRRPSVPTGSPTRKPSASNSTGIIPIVAILI 194
 QY 219 FPGICLL--SLPTGLMRYQRMKS-----KLYSIYCGKSTPEKEG----- 257
 DB 195 LTVICTIVGAILF--LKRRQROOSETNGNLEEVKVIDECPRSEEGEENRNAGLEKEE 251
 QY 258 -----ELEGTTK-----PLAPNPSFSP--GTPPT 282
 DB 252 EHPESRPLLTQETQETGSKSIPVEDEDRGIDSLPKHNOLFKRPSLSALPQNHMGFT-- 309
 QY 283 LGFSVPVSSFTSSSTYTPGDCPNFAAPRREVAPPY-OGADPILATALASDPIN--PL 336
 DB 310 --VDPAP-----RPRDRT-----EIRLNHGKGD-----DP-PRKLLPL 341
 QY 339 QKWEDSAHKPQSLDTPDPATLYAVENVPLRW-KEFVRLGLSDHEIDRLONGRCCLR 397
 DB 342 LGEEESLSK--SFDLFDLSL-----DVRYHNKFRFSGVSDNSIKLAETQOP--M 386
 QY 398 EAOYSMLATWRRTPRREATLELGRVLRMD 429
 DB 387 DKVYDLRWVMQKEGLR-ANINTLLQALDLD 417
 RESULT 10
 Q9DF34 PRELIMINARY; PRT; 357 AA.
 AC Q9DF34;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
 DE Death receptor.
 OS Brachydanio rerio (Zebrafish) (zebra danio).

Query Match	8.5%	Score 211	DB 13	Length 357
Best Local Similarity	27.1%	Pred. No. 2.1e-10		
Matches 62	Conservative 32	Mismatches 83	Indels 52	Gaps 10

RESULT 11	
Q62327	
ID Q62327	PRELIMINARY;
	PRT; 459 AA

DT 01-NOV-1996 (TREMBLrel. 01, created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Murine tumour necrosis factor receptor 2 protein (Fragment).
GN TNFRSF1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RC Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.",
RL Genomics 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RC MEDLINE=95178848; PubMed=7873884;
RX Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene";
RL Mamm. Genome 5:726-727(1994).

Query Match	8.28;	Score 204.5;	DB 11;	Length 459;
Best Local Similarity	23.78;	Pred. No. 1e-09;		
Matches 83;	Conservative 43;	Mismatches 145;	Indels 79;	Gaps 15

RESULT 12	
088734	
ID 088734	PRELIMINARY; PRT; 482 AA

DT	01-NOV-1998 (TReMBLrel. 08, Created)
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE	P80 TNF-alpha receptor.
GN	TNFR2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98414512; PubMed=9740674;
RA	Hurle B., Segade F., Rodriguez R., Ramos S.S., Iazo P.S.;
RT	"The Mouse Tumor Necrosis Receptor 2 Gene: Genomic Structure and Characterization of the two Transcripts."
RL	Genomics 52:79-98(1998).
DR	EMBL: Y14619; CAA74969.1; -
DR	EMBL: Y14620; CAA74969.1; JOINED.
DR	EMBL: Y14621; CAA74969.1; JOINED.
DR	EMBL: Y14622; CAA74969.1; JOINED.
DR	EMBL: Y14623; CAA74969.1; JOINED.
DR	EMBL: Y14679; CAA74969.1; JOINED.
DR	HSSP: P19438; INCE.


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RESULT 15

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE B-type Fas antigen.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
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RA Isono T., Tanabe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB021298; BAA78430.1; -.
DR HSSP: P25443; 1DDF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
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Query Match 7.6%; Score 189; DB 6; Length 319;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:14:10 ; Search time 65 seconds
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Title: US-09-899-429A-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1368	100.0	1368	10	US-09-899-422-1
4	1368	100.0	2141	9	US-09-898-234-16
5	1368	100.0	2141	9	US-09-899-429A-26
6	1368	100.0	2111	10	US-09-899-422-16
7	1366.4	99.9	2111	10	US-09-880-107-2360
8	1366.4	99.9	2175	12	US-10-120-397-1
9	1122	82.0	1334	9	US-09-898-234-11
10	1122	82.0	1334	10	US-09-899-422-11
11	1117.2	81.7	1334	9	US-09-899-429A-21
12	743.4	54.3	2130	10	US-09-917-800A-1601
13	735.4	53.8	2173	9	US-09-898-234-14
14	735.4	53.8	2173	9	US-09-899-429A-24
15	735.4	53.8	2173	10	US-09-899-422-14
16	685.4	50.1	2440	10	US-09-970-532-1
17	633	46.3	633	9	US-09-899-429A-7
18	603	44.1	603	9	US-09-899-429A-13
19	557	40.7	600	9	US-09-899-429A-11

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21	527	38.5	570	9	US-09-899-429A-17	Sequence 17, Appl
22	516	37.7	519	9	US-09-899-429A-15	Sequence 15, Appl
23	514	37.6	1301	10	US-09-756-186-7	Sequence 7, Appl1
24	513	37.5	516	9	US-09-899-429A-19	Sequence 19, Appl
25	506	37.0	1147	10	US-09-756-186-5	Sequence 5, Appl1
26	483	35.3	483	9	US-09-898-234-3	Sequence 3, Appl1
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28	483	35.3	483	10	US-09-899-422-3	Sequence 3, Appl1
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33	337	24.6	427	10	US-09-876-589-236	Sequence 236, App
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35	329.6	24.1	5870	10	US-09-838-718A-8	Sequence 8, Appl1
36	140.4	10.3	158	9	US-09-898-234-66	Sequence 68, Appl
37	140.4	10.3	158	9	US-09-899-422-68	Sequence 68, Appl
38	134	9.8	158	9	US-09-899-429A-78	Sequence 78, Appl
39	124.4	9.1	413	10	US-09-960-352-2885	Sequence 2885, Ap
40	123.2	9.0	151	9	US-09-898-234-20	Sequence 20, Appl
41	123.2	9.0	151	9	US-09-899-429A-30	Sequence 30, Appl
42	123.2	9.0	151	10	US-09-899-422-20	Sequence 20, Appl
43	98.2	7.2	154	10	US-09-783-590-8601	Sequence 8601, Ap
44	87	6.4	87	9	US-09-898-234-5	Sequence 5, Appl1
45	87	6.4	87	10	US-09-899-422-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-898-234-1
Sequence 1, Application US/09898234
Patent No. US2002015112A1
GENERAL INFORMATION:
APPLICANT: Hauptmann, Rudolph
APPLICANT: Haumer, Adolph
APPLICANT: Mauner-Fogy, Ingrid
APPLICANT: Stralow, Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
FILE REFERENCE: 98,385-I
CURRENT APPLICATION NUMBER: US/09/898,234
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/525,998
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
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NAME/KEY: sig_peptide
LOCATION: (1)..(87)
NAME/KEY: misc_feature
LOCATION: (88)..(120)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
OTHER INFORMATION: extracellular proteases following secretion.
NAME/KEY: misc_feature
LOCATION: (606)..(633)
OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by


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: Sequence 26, Application US/09899429A
: Patent No. US20020169118A1
: GENERAL INFORMATION:
: APPLICANT: Hauptmann, Rudolph
: APPLICANT: Hammler, Adolph
: APPLICANT: Maurer-Fegy, Ingrid
: APPLICANT: Stralowa, Christian
: TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
: TITLE OF INVENTION: Them
: FILE REFERENCE: 98-385-J
: CURRENT APPLICATION NUMBER: US/09/899,429A
: PRIOR FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: 09/792,356
: PRIOR FILING DATE: 2000-02-23
: PRIOR APPLICATION NUMBER: 08/477,639
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/383,676
: PRIOR FILING DATE: 1995-02-01
: PRIOR APPLICATION NUMBER: 08/153,287
: PRIOR FILING DATE: 1993-11-17
: PRIOR APPLICATION NUMBER: 07/821,750
: PRIOR FILING DATE: 1992-01-02
: PRIOR APPLICATION NUMBER: 07/511,430
: PRIOR FILING DATE: 1990-04-20
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 26
: LENGTH: 2141
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: human TNF-R 1n
: OTHER INFORMATION: LTNF-R2
: NAME/KEY: CDS
: LOCATION: (213)..(1577)
: US-09-899-429a-26

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
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; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
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; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2360
; LENGTH: 2111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M58286
US-09-880-107-2360

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Best Local Similarity 99.9%:  Pred. No. 0:
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Db 187 ATGGGCGCTCTCCACCGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
Qy 61 GGAATATACCCCTCAGGGGTTATTGAGCTGTCCCTCACCCTAAGGGGACAGAGAGAGA 120
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Db 367 AATGGCCAAAGAGAACTACTTGTACAAATGACTGTCCAGGCCCGGGGAGATACGAGAC 426
Qy 241 TCGAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTTC 300
Db 427 TCGAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCTTC 486
Qy 301 AGCTGCTCCAAATCCGGAAGGAAATGGTTCAGGTGGAATCTCTTGTGCACAGTGGAC 360
Db 487 AGCTGCTCCAAATCCGGAAGGAAATGGTTCAGGTGGAATCTCTTGTGCACAGTGGAC 546
Qy 361 CCGGACACCGGTGTGTGCTGACAGAGAAACAGTACCGGCATTTATGGAGTGAACCTT 420
Db 547 CCGGACACCGGTGTGTGCTGACAGAGAAACAGTACCGGCATTTATGGAGTGAACCTT 606
Qy 421 TTCAGTGTCTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480
Db 607 TTCAGTGTCTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 666
Qy 481 AAACAGAACACCGTGTGACCTGTGCATGCAAGTTTCTTTCTAAGAGAAAACGAGTGTTC 540
Db 667 AAACAGAACACCGTGTGACCTGTGCATGCAAGTTTCTTTCTAAGAGAAAACGAGTGTTC 726
Qy 541 TCCTGTAGTAAGTAAGAAAAGCCGTGGATGACAGCAAGTTTGGCTTACCCTGATTTGAG 600
Db 727 TCCTGTAGTAAGTAAGAAAAGCCGTGGATGACAGCAAGTTTGGCTTACCCTGATTTGAG 786
Qy 601 AATGTTAAGGACAGTGAAGACACAGCAGTGTGCTTGTGCTTGTGCTTGTGCTTGTG 660
Db 787 AATGTTAAGGACAGTGAAGACACAGCAGTGTGCTTGTGCTTGTGCTTGTGCTTGTG 846
Qy 661 GGTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTAAATGATGCTTACCAAGGTGGAAG 720
Db 847 GGTCTTTGCTTTTATCCCTCTCTTCAATTTGTTTAAATGATGCTTACCAAGGTGGAAG 906
Qy 721 TCCAACTTACTCCATTTTGTGTGGAAATGACACCTGAAAAGAGGGAGCTTGA 780
Db 907 TCCAACTTACTCCATTTTGTGTGGAAATGACACCTGAAAAGAGGGAGCTTGA 966
Qy 781 GGAAGTACTAAGAGCCCTGGGCCCCAAGCCAGCTTGTGCTTGTGCTTGTGCTTGTG 840
Db 967 GGAAGTACTAAGAGCCCTGGGCCCCAAGCCAGCTTGTGCTTGTGCTTGTGCTTGTG 1026
```

QY	841	CCCAACCCGGGGCTTGA	GTCCCGTGGCCAGTGCACCTTACCTCCAGGCTCCACCACTATAC	900
Dp	1027	CCCAACCCGGGGCTTCA	TCCCGTGGCCAGTGCACCTTACCTCCAGGCTCCACCACTATAC	1086
QY	901	CCCAGTACTGTCCCACT	TTTGGGGCTCCCGAGAGAGTGGACCAACCTTACAGGG	960
Dp	1087	CCCGTGACTGTCCCAACT	TTTGGGGCTCCCGAGAGAGTGGACCAACCTTACAGGG	1146
QY	961	GCTAACCCCATCTTGT	GAGACGCTCGCTCCGACCCATCCCAACCCCTTACAG	1020
Dp	1147	GCTAACCCCATCTTGT	GAGACGCTCGCTCCGACCCATCCCAACCCCTTACAG	1206
QY	1021	TGGGAGACAGCGCCCA	CAAGCCACAGAGCTTAGACACTGATGACCCCGACGCTGAC	1080
Dp	1207	TGGGAGACAGCGCCCA	CAAGCCACAGAGCTTAGACACTGATGACCCCGACGCTGAC	1266
QY	1081	GCCGTGGTGGAGAACT	GTCCCGCTTGGCTGGAAAGTAATTCGTGCGCGCTTAGGGCTG	1140
Dp	1267	GCCGTGGTGGAGAACT	GTCCCGCTTGGCTGGAAAGTAATTCGTGCGCGCGCTTAGGGCTG	1326
QY	1141	AGGCACACACAGATCG	ATGCGCTGGAGCTGCAGAAAGGCGCTGCTCGCGAGGCGCA	1200
Dp	1327	AGGCACACACAGATCG	ATGCGCTGGAGCTGCAGAAAGGCGCTGCTCGCGAGGCGCA	1386
QY	1201	TACAGCATGTGTGCGAC	CTTGAGGCGGCACAGCGCGGAGAGCCACAGCTGGAGCTG	1280
Dp	1387	TACAGCATGTGTGCGAC	CTTGAGGCGGCACAGCGCGGAGAGCCACAGCTGGAGCTG	1446
QY	1261	CTGGGACGCTGTCTCG	CGCATGACCTGTGGCTGTCTGGAGACATCGAGAGGCG	1320
Dp	1447	CTGGGACGCTGTCTCG	CGCATGACCTGTGGCTGTCTGGAGACATCGAGAGGCG	1506
QY	1321	CTTTGGGGCGCGCGCG	CTTCCCGCGCGGCCACAGCTTCTAGATGA	1368
Dp	1507	CTTTGGGGCGCGCGCG	CTTCCCGCGCGGCCACAGCTTCTAGATGA	1554

RESULT 8
US-10-120-397-1
Sequence 1, Application US/10120397
Patent No. US20020142357A1
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BRAEBROSCCH, Cord
TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/120,397
FILING DATE: 12-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/054,970
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

:	TELEX: 248633
:	INFORMATION FOR SEQ ID NO: 1:
:	SEQUENCE CHARACTERISTICS:
:	LENGTH: 2175 base pairs
:	TYPE: nucleic acid
:	STRANDEDNESS: single
:	TOPOLOGY: linear
:	MOLECULE TYPE: cDNA
:	FEATURE:
:	NAME/KEY: CDS
:	LOCATION: 256..1620
:	SEQUENCE DESCRIPTION: SEQ ID NO: 1:
:	US-10-120-397-1
:	
:	Query Match
:	Best Local Similarity 99.9%; Score 1366.4; DB 12; Length 2175;
:	Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY	1 ATGGGCGCTCCACCGTGCCTGACCTGTCTGTCTGCACTGTGTCCTCTGAGCTGTTGGTG 60
DB	256 ATGGGCGCTCCACCGTGCCTGACCTGTCTGTCTGCACTGTGTCCTCTGAGCTGTTGGTG 315
QY	61 GGAATATACCCTCAGGGGGTTATTGGACTGTGCCCTCACCTTAGGGGACAGGAGAAGANA 120
DB	316 GGAATATACCCTCAGGGGGTTATTGGACTGTGCCCTCACCTTAGGGGACAGGAGAAGANA 375
QY	121 GATAGTGTGTGCCCAAGAAATATATATCATCCCTCAAATAATTCGATTGTGTATAC 180
DB	376 GATATGTGTGTCCCCAAGAAATATATATCATCCCTCAAATAATTCGATTGTGTATAC 435
QY	181 AAGTCCCAAAAAGAACCTACTTGTACATATGACTGTCCAAGCCCGGGGAGATACGGAC 240
DB	436 AAGTCCCAAAAAGAACCTACTTGTACATATGACTGTCCAAGCCCGGGGAGATACGGAC 495
QY	241 TGCAGGGAGTGTGAAGGGGCTCTTCAACCGCTTCAGAAAAACAGCTCAGACTGGCTC 300
DB	496 TGCAGGGAGTGTGAAGGGGCTCTTCAACCGCTTCAGAAAAACAGCTCAGACTGGCTC 555
QY	301 AGCTGCTCCAAATGCGGAAAGGAATGGGTCAAGTGTCTTTTGGACAAGTGAC 360
DB	556 AGCTGCTCCAAATGCGGAAAGGAATGGGTCAAGTGTCTTTTGGACAAGTGAC 615
QY	361 CGGGACACCGTGTGGGTGCGAGAAAGAACCGTACCGGCAATTATTGGAGTAAGAAACCTT 420
DB	616 CGGGACACCGTGTGGGTGCGAGAAAGAACCGTACCGGCAATTATTGGAGTAAGAAACCTT 675
QY	421 TTCCAGTCTTCAATTGGACGCTCTGCTTCAATGGGACCGTGACACTCTCTCTGCCAGGAG 480
DB	676 TTCCAGTCTTCAATTGGACGCTCTGCTTCAATGGGACCGTGACACTCTCTCTGCCAGGAG 735
QY	481 AAACGAAACACCGTGTGACACCTGCATCAGGTTTTCTTTCTPAAGAAAGACAGTGTGC 540
DB	736 AAACGAAACACCGTGTGACACCTGCATCAGGTTTTCTTTCTPAAGAAAGACAGTGTGC 795
QY	541 TCCTGTACTACTGTAAACAAAAGCCGTGAGAGTGACAGAAAGTGTGCTTACCCAGATTGAG 600
DB	796 TCCTGTACTACTGTAAACAAAAGCCGTGAGAGTGACAGAAAGTGTGCTTACCCAGATTGAG 855
QY	601 AATGTTAAGGCACTGAGAGCTCAGGACACACAGTGTGTTGCCCTGTCTATTTTCTTT 660
DB	856 AATGTTAAGGCACTGAGAGCTCAGGACACACAGTGTGTTGCCCTGTCTATTTTCTTT 915
QY	661 GGTCCTTCCCTTTAATGCCCTCCTCTTCAATGGGTTAAATGATACGTACCAACGGTGAAG 720
DB	916 GGTCCTTCCCTTTAATGCCCTCCTCTTCAATGGGTTAAATGATACGTACCAACGGTGAAG 975
QY	721 TCCAAGCTCTACTCCATTGTTTGGGAATTCAGACACTGAAAAAGAGGGGAGCTTGAA 780
DB	976 TCCAAGCTCTACTCCATTGTTTGGGAATTCAGACACTGAAAAAGAGGGGAGCTTGAA 1035
QY	781 GGAACCTACTAAGAGCCCTGGCCCCCAAAACCAAGCTTCAAGTCCCACTCCAGCTTCAC 840
DB	1036 GGAACCTACTAAGAGCCCTGGCCCCCAAAACCAAGCTTCAAGTCCCACTCCAGCTTCAC 1095

Qy	841	CCCAACCTGGGGCTTCAAGTCCCGGCGCCAGTTGCAGCTTACCTCCAGCTCCACCTATAC	900
Db	1096	CCCACTCTGGGGCTTCAAGTCCCGGCGCCAGTTGCAGCTTACCTCCAGCTCCACCTATAC	1155
Qy	901	CCCGGTACAGTGTCCCAACTTTGGGGGTCCCGGAGAGAGTGGGCAACCCATACAGGGG	960
Db	1156	CCCGGTACAGTGTCCCAACTTTGGGGGTCCCGGAGAGAGTGGGCAACCCATACAGGGG	1215
Qy	961	GCATTACCCCATCTCTTGGGAGACAGCCCTCGGCTCCGAGACCCATCCCAACCCCTTCAGAG	1020
Db	1216	GCATTACCCCATCTCTTGGGAGAGCCCTCGGCTCCGAGACCCATCCCAACCCCTTCAGAG	1275
Qy	1021	TGGGAGAGACAGCGCCCAACAAGCACAGAGCCTTAGACACTGATGACCCCGAGACGCTTAC	1080
Db	1276	TGGGAGAGAGACAGCGCCCAACAAGCACAGAGCCTTAGACACTGATGACCCCGAGACGCTTAC	1335
Qy	1081	GCCCTGGTGGAGAAACGTGCCCCCGCTTGGGCTGGAGGAATTTGTGCGCGCTTAGGGCTG	1140
Db	1336	GCCCTGGTGGAGAAACGTGCCCCCGCTTGGGCTGGAGGAATTTGTGCGCGCTTAGGGCTG	1395
Qy	1141	AGGCACACAGAGATCGATGGGCTGGAGAGTGCAGAAACGGGCGTGGCTCGGAGAGGCCAA	1200
Db	1396	AGGCACACAGAGATCGATGGGCTGGAGAGTGCAGAAACGGGCGTGGCTCGGAGAGGCCAA	1455
Qy	1201	TACAGCATGCTGGGCGAAGTTGGAGGCGGCGCACGCGCGCGAGAGGCACACTGGAGCTG	1260
Db	1456	TACAGCATGCTGGGCGAAGTTGGAGGCGGCGCACGCGCGCGAGAGGCACACTGGAGCTG	1515
Qy	1261	CTGGGAGCGGTGCTCCGCGACATGAGACCTGTGGGCTGCTGGAGACATCGAGAGGCG	1320
Db	1516	CTGGGAGCGGTGCTCCGCGACATGAGACCTGTGGGCTGCTGGAGACATCGAGAGGCG	1575
Qy	1321	CTTTGGCGGGCGCGCGCCCTCCCGCGGGCCAGCTTCTCAAGTGA	1368
Db	1576	CTTTGGCGGGCGCGCGCCCTCCCGCGGGCCAGCTTCTCAAGTGA	1623

```

1 RESULT 9
2 US-09-898-234-11
3 ; Sequence 11, Application US/09898234
4 ; Patent No. US2002015112A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Hauptmann, Rudolph
7 ; APPLICANT: Himmelr, Adolfh
8 ; APPLICANT: Maurer-Fogy, Ingrid
9 ; APPLICANT: Stracova, Christian
10 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
11 ; TITLE OF INVENTION: Them
12 ; FILE REFERENCE: 98, 385-I
13 ; CURRENT APPLICATION NUMBER: US/09/898,234
14 ; CURRENT FILING DATE: 2001-07-03
15 ; PRIOR APPLICATION NUMBER: 09/525, 998
16 ; PRIOR FILING DATE: 2000-03-15
17 ; PRIOR APPLICATION NUMBER: 08/383,676
18 ; PRIOR FILING DATE: 1995-02-01
19 ; PRIOR APPLICATION NUMBER: 08/153,287
20 ; PRIOR FILING DATE: 1993-11-17
21 ; PRIOR APPLICATION NUMBER: 07/821,750
22 ; PRIOR FILING DATE: 1992-01-02
23 ; PRIOR APPLICATION NUMBER: 07/511,430
24 ; PRIOR FILING DATE: 1990-04-20
25 ; NUMBER OF SEQ ID NOS: 87
26 ; SOFTWARE: Patentin Ver. 2.0
27 ; SEQ ID NO 11
28 ; LENGTH: 1334
29 ; TYPE: DNA
30 ; ORGANISM: Artificial Sequence
31 ; FEATURE:
32 ; NAME/KEY: CDS
33 ; LOCATION: (213)..(1325)
34 ; OTHER INFORMATION: Description of Artificial Sequence: cdna insert of
35 ; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors

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US-09-898-234-11

Query Match	82.0%;	Score 112:	DB 9;	Length 1334;
Best Local Similarity	100.0%;	Pred. No. 4e-276;		
Matches 112:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Qy	1021	TGGGAGGACAGCGCCCAACGAGCGCTTAC	1080
Db	1233	TGGGAGGACAGCGCCCAACGAGCGCTTAC	1292
Qy	1081	GCGGTGTGAGAACTGCCCCGTTGCGGTGAGAAATTC	1122
Db	1293	GCGGTGTGAGAACTGCCCCGTTGCGGTGAGAAATTC	1334

RESULT 10
US-09-899

Sequence 11, Application US/0989422
 Patent No. US20020090676A1
 GENERAL INFORMATION:
 APPLICANT: Hauptmann, Rudolph
 APPLICANT: Hammler, Adolph
 APPLICANT: Maurer-Poggy, Ingrid
 APPLICANT: Stratowa, Christian
 TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 TITLE OF INVENTION: Them
 FILE REFERENCE: 98,385-H
 CURRENT APPLICATION NUMBER: US/09/899,422
 CURRENT FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: 09/525,998
 PRIOR FILING DATE: 2000-03-15
 PRIOR APPLICATION NUMBER: 08/383,676
 PRIOR FILING DATE: 1995-02-01
 PRIOR APPLICATION NUMBER: 08/153,287
 PRIOR FILING DATE: 1993-11-17
 PRIOR APPLICATION NUMBER: 07/821,750
 PRIOR FILING DATE: 1992-01-02
 PRIOR APPLICATION NUMBER: 07/511,430
 PRIOR FILING DATE: 1990-04-20
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 11
 LENGTH: 1334
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (213)..(1325)
 OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
 OTHER INFORMATION: lambdaTNF-BP1s and pTNF-BP1s vectors
 US-09-899-422-11

Query Match	82.0%;	Score 1122;	DB 10;	Length 1334;
Best Local Similarity	100.0%;	Pred. No. 4e-276;		
Matches 1122;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	ATGGCCCTC	CACGCGCC	GGACCTG	CTGTG	GCACATG	GGTCC	GTGGAGCTG	GTG	60
Db	213	ATGGCCCTC	CTCACC	GTGCTG	ACCTG	CTCTGTG	CTCCACTG	GTGCTCC	GTGGAGCTGTG	272
QY	61	GGAATATAT	ACCCCTC	AGGGGTT	ATTATG	AGCTG	TGCTCC	TACCTAG	GGGACAGGAGAA	120
Db	273	GGAATATAT	ACCCCTC	CAGGGGTT	ATTATG	AGCTG	TGCTCC	TACCTAG	GGGACAGGAGAA	332
QY	121	GATAGTGTG	TCTCCCA	AGGAAATAT	ATCCACC	CTCAAA	TATATTC	GATTTG	CTGTACC	180
Db	333	GATAGTGTG	TCTCCCA	AGGAAATAT	ATCCACC	CTCAAA	TATATTC	GATTTG	CTGTACC	332
QY	181	AAGGCCA	CAAGGAAC	CTCTTGT	TACAA	TAGCTG	TCAGGCCC	GGGGG	CAGGATAC	240
Db	393	AAGGCCA	CAAGGAAC	CTCTTGT	TACAA	TAGCTG	TCAGGCCC	GGGGG	CAGGATAC	452
QY	241	TGCAGGAG	AGTGTG	AGAGCGG	CTCTTCA	CCGCTT	CAAAAA	ACCACCT	CAACACTG	300
Db	453	TGCAGGAG	AGTGTG	AGAGCGG	CTCTTCA	CCGCTT	CAAAAA	ACCACCT	CAACACTG	512
QY	301	AGCTGCTC	CAATGC	CGAAAGAA	TGGGTAC	AGGTG	GAGATCT	CTTCTT	GCACAGT	360
Db	511	AGCTGCTC	CAATGC	CGAAAGAA	TGGGTAC	AGGTG	GAGATCT	CTTCTT	GCACAGT	672

D	b	513	AGTGTCCAAATTCGGAAAGAAATGGGTGACGTGGAAATCTCTTCTTGACACTGGAC	572
O	y	361	CGGACACCGTGTGTGCTCGAGAGAACACAGTACCGGCATTTATTTGAGTGAACCTT	420
D	b	573	CGGGACACCGTGTGTGCTCGAGAGAAACACAGTACCGGCATTTATTTGAGTGAACCTT	632
O	y	421	TTCCAGTCTCAATTGACGTCTGTGCTCAATGGAGCGGTGACCTCTCCGACAGAG	480
D	b	633	TTCCAGTCTCAATTGACGTCTGTGCTCAATGGAGCGGTGACCTCTCTGCGACAGAG	692
O	y	481	AAACAGAACCCGTGTGCTGACCTGCGCAATGACAGTGTTCCTTAAGAGAAAAACGAGTGTCTC	540
D	b	693	AAACAGAACCCGTGTGCTGACCTGCGCAATGACAGTGTTCCTTAAGAGAAAAACGAGTGTCTC	752
O	y	541	TTCTGTACTAATCTAAGAAAAGCTGTGAGTGCACAGATTGTGCTTACCCAGATTGAG	600
D	b	753	TTCTGTACTAATCTAAGAAAAGCTGTGAGTGCACAGATTGTGCTTACCCAGATTGAG	812
O	y	601	AATGTTAAGGACACTGAGGACTGAGGACACAGTGTCTGTGGCCCTGGTCATTTTCTTT	660
D	b	813	AATGTTAAGGACACTGAGGACTGAGGACACAGTGTGTATGCTGTACCAAGGTGAGAG	720
O	y	661	GGTCTTGTGCTTTATTCCTCCTCTCTCATTTGTTTATGTATGCTGTACCAAGGTGAGAG	720
D	b	873	GGTCTTGTGCTTTATTCCTCCTCTCTCATTTGTTTATGTATGCTGTACCAAGGTGAGAG	932
O	y	721	TTCCAACTACTACTCATTTGTTTGTGGAAATGCACACCTGAAAAAGAGGGGAGCTTGA	780
D	b	933	TTCCAACTACTACTCATTTGTTTGTGGAAATGCACACCTGAAAAAGAGGGGAGCTTGA	992
O	y	781	GGAACTACTACTAAGCCCTGGGGCCCAAAACCAAGTGTAGTCCACTGCAGCTTCAC	840
D	b	993	GGAACTACTACTAAGCCCTGGGGCCCAAAACCAAGTGTAGTCCACTGCAGCTTCAC	1053
O	y	841	CCCACTCTGGGCTTCAGTCCCGTGGCCAGTTCCACCTTCACCTGCAGCTTCACCTATAC	900
D	b	1053	CCCACTCTGGGCTTCAGTCCCGTGGCCAGTTCCACCTTCACCTGCAGCTTCACCTATAC	1112
O	y	901	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGGAGAGAGTGGCACACCTATAGAGG	960
D	b	1113	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGGAGAGAGTGGCACACCTATAGAGG	1172
O	y	961	GCTACCCCATCTCTTGGGAGACGCCCTGCTCCGACCCCATCCCAACCCCTCTCAGAG	1020
D	b	1173	GCTACCCCATCTCTTGGGAGAGGCCCTGCTCCGACCCCATCCCAACCCCTCTCAGAG	1233
O	y	1021	TGGGAGGACACGCGCCCAACAAGCCACAGAGCTTAGACATGATGACCCCGGAGCGCTGAC	1080
D	b	1233	TGGGAGGACACGCGCCCAACAAGCCACAGAGCTTAGACATGATGACCCCGGAGCGCTGAC	1292
O	y	1081	GCGTGTGTGGAGAACGTGCCCCGCTTGGCTGTGGAAAGAAATTC	1122
D	b	1293	GCGTGTGTGGAGAACGTGCCCCGCTTGGCTGTGGAAAGAAATTC	1334

RESULT 11
US-09-899-429A-21

```

: Sequence 21, Application US/09899429A
: Patent No. US20020169118A1
:
: GENERAL INFORMATION:
:   APPLICANT: Hauptmann, Rudolph
:   APPLICANT: Himmeler, Adolph
:   APPLICANT: Maurer-Fogy, Ingrid
:   APPLICANT: Strataowa, Christian
:   TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
:   TITLE OF INVENTION: Them
:   FILE REFERENCE: 98-385-J
:   CURRENT APPLICATION NUMBER: US/09/899,429A
:   CURRENT FILING DATE: 2001-07-03
:   PRIOR APPLICATION NUMBER: 09/792,356
:   PRIOR FILING DATE: 2000-02-23
:   PRIOR APPLICATION NUMBER: 08/477,639
:   PRIOR FILING DATE: 1995-06-07

```


D	b	365	GATAAATTGTGTGTCGCCAGGGGAAGTATGGCCATCCAAAGAAATATATTCATCTGCTGCACC	424
O	y	181	AAGTGCACAAGAGAACCTTACTTGTACAAATGACTGTCCAGGCCCGGGGCGAGGATACGGAC	240
D	b	425	AAGTGCACAAGAGAACCTTACTTGTGAGTGAAGTCTCCAAAGCCCGAGGCGAGGAACAGTGC	484
O	y	241	TGCAGGGAGTGTAGAGCGGCTCCTTCACCCGCTTCAGAAAACCACTCAGACACTGCTC	300
D	b	485	TGCGAGGTCTCTCATTAAGAGCACCTTTTACAGCTTCGCAAMACACGTGACAGACAGTGTCTC	544
O	y	301	AGCTGTCTCAAAATGCGCAAAAGAAATGGGTCAGGTGGAGTATCTCTTGTGCACAGTGGAC	360
D	b	545	AGTTGTCAGAGACATGTGCGGAAAGAAATGTTCACAGTGTGAGATATTTCTCTTGCAAAAGCTAC	604
O	y	361	CGGAGACACCGTGTGTGGCTCAGGAAAGAACACAGTACCGGCAATTTATGGAGTGAAGAACTT	420
D	b	605	ATGGACACCGTGTGTGGCTCAGGAAGAAACCAATTCACAGCGTACCTGATGTGAGACGAT	664
O	y	421	TTTCAATGCTTCAATTGTCAGCCTCTGCTTCATGGAGCCGTGCACCTCTCCTGCGCAGAG	480
D	b	665	TTTCAAGTGTGTGAGCTGCACCCCTCTTCAATGGAGCCGTGACAAATCCCTGTAAAGAG	724
O	y	481	AAACAGAAACACCGTGTGCACCTGCAATGGAGGTTTCTTTCTAAGAGAAACAGAGGTGTC	540
D	b	725	AAACAGAAACACCGTGTGTACTGTCCACAGCGATTTCTTTCTAAGGGGAAATGAGTGACC	784
O	y	541	TCTGTGTAGTAACTGTAAAGAAACCTGAGGTGACAGAAATTTGTGCTTACCCAGATTAG	600
D	b	785	CTTTGCAAGCCACTGTCAAGAAATAATCAAGAAATGATATGAACTGTGGCTTACCTGCATTTGCA	844
O	y	601	AATGTTAAGGGGACTGTAGGACTCAGGACACACAGTGTGTCCTCCCTGTCATTTTCTTT	660
D	b	845	AATGTCAAAACCCCGAGGACTCAGGTACTGCGGTGCTGTGCTGCTGTGTTATCTTCTCTA	904
O	y	661	GGTCTTGGCCTTTATATCCGCTCTTCATTTGGTTAATGTATGCTACCAACGGGTGAG	720
D	b	905	GGCTTTGGCCTTTATTTATCTTATCTGTGATAGTCTATGCTGCGATATCCCAAGTGGAG	964
O	y	721	TCCAAAGCTTACTTCATTGTTGTGGGAAATGCACACCTGAAAGAGAGGGAGCTTAA	780
D	b	965	CCCAAGGCTTACTCATCTATTTGTAAAGGATTCAGTCTCCGTGCAAGAGAGGTGAGGGTCAA	1024
O	y	781	GGAACTTACTTAAAGCCCCCT-----GGCCCCAAACCCAAAGCTTACGTCCACTCCAGGC	834
D	b	1025	GGAAATTTGTACTAAGCCCCCTTAACTCCAGGCTTATCCAGCTTACAGCCCCAACCCCGGC	1084
O	y	835	TTTCAACCCCAACCCGTGGGCTTCACTCCCGTGGCCAG-----TTCCACACTTC	879
D	b	1085	TTTCAACCCCACTGTGGGCTTTCACACACCCCAAGCTTCAAGTCAATCTGTCTCAGTAC	1144
O	y	880	ACCTTCAGCTTCACTTATTTATCCCGGAGATGTCCCAATTTTGGCGGCTCCCGCAGAGAG	939
D	b	1145	CCCATCAGAGCCCGCTTTCGGTCTTAACTGGCACAACTTGTGTGCACCTTAAAGAGAG	1204
O	y	940	GTGGACACACCTTATCAGAGGGGGGTGACCCCATCTTTGGACAGCCCTGCGCTCCGACCC	999
D	b	1205	GTGGTCCCAACCC---CAGGGTGTCTGACCCCTCTCTCTTACGATATCCCTCAACCCGTMGCA	1261
O	y	1000	ATCCCCCAACCCCTTTCAGAAAGTGGGAGAG---CAGCGCCCAACAGCCACAGAGCTTAAC	1056
D	b	1262	ATCCCCCGCCCTGTGTGCGAAATGGGAAGAGTGTGTGCGGGCCAGCAACAGGCTTTAC	1321
O	y	1057	ACTGATGACCCCGGAGAGCTGTACGCGGTGTGGAGAACGTGGCCCCCGTGTGGGTGGAG	1118
D	b	1332	ACTGCAGACCTTGTGAGTGTGTATGCTGTGTGTGAGATGGCGTGTCTCCACACAGCTTGGAG	1381
O	y	1117	GAATTTGTGGGGCGCCTTAAAGGCTTGAAGGACACAGAGATGATTCGGCTGTGAGCTGCAGAC	1178
D	b	1382	GAGTTTATGCGGGGCTTCGTGGGGGTGAGGAGACAGAGATGAGAGGGTGTGAGCTGCAGAC	1441
O	y	1177	GGGGGCTGTGCTGGCGCAGAGGCGCAATACGATGTCTGTGGCACTCGAGAGGGCGCACGGC	1236
D	b	1442	GGGGGTTTCTTCCCGCGAGGCTCATTTACAGATATCTTGAAGCTGTGGGGCGCGCACGGC	1501

QY	1237	CGGGCGAGGCGCACGCGAGAGCGCTCGGACGAGTGGACCTGCTGGG	1296
QY	1237	CGGGCGAGGCGCACGCGAGAGCGCTCGGACGAGTGGACCTGCTGGG	1296
Db	1502	CGACACGAGGCGCACGCTGGACGCTAGTGGCGCGCGCTGTTTGGCAGTCAAGAACTGCTGGCG	1561
QY	1237	TGCTCGAGAGCATCGAGAGGCGCTTTTGGCGGCGCCGCC	1335
Db	1552	TGCTCGAGAGAACATCCGCGAGACTCTTAGAAAGCCCTGCC	1600

RESULT 14
US-09-899-429A-24
: Sequence 24, Application US/09899429A
: patent No. US20020169118A1

```
?
? APPLICANT: Hauptmann, Rudolph
?
? APPLICANT: Himmeler, Adolph
?
? APPLICANT: Maurer-Fogy, Ingrid
?
? APPLICANT: Strawowa, Christian
?
? TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
?
? TITLE OF INVENTION: Them
```

```

1 CURRENT APPLICATION NUMBER: US-09/899,432A
2 CURRENT FILING DATE: 2001-07-03
3 PRIOR APPLICATION NUMBER: 09/792,356
4 PRIOR FILING DATE: 2000-02-23
5 PRIOR APPLICATION NUMBER: 08/477,639
6 PRIOR FILING DATE: 1995-06-07
7 PRIOR APPLICATION NUMBER: 08/383,676
8 PRIOR FILING DATE: 1995-02-01
9 PRIOR APPLICATION NUMBER: 08/153,287
10 PRIOR FILING DATE: 1993-11-17
11 PRIOR APPLICATION NUMBER: 07/821,750
12 PRIOR FILING DATE: 1992-01-02
13 PRIOR APPLICATION NUMBER: 07/511,430
14 PRIOR FILING DATE: 1990-04-20
15 NUMBER OF SEQ ID NOS: 97
16 SOFTWARE: Patentin Ver. 2.0

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; SEQ ID NO 24
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; LENGTH: 2173
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; TYPE: DNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: ratNF-R8
;
; NAME/KEY: CDS
;
; LOCATION: (245) .. (1627)
;
; US-09-899-429A--24

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Query Match	53.8%	Score 735.4	DB 9	Length 2173
Best Local Similarity	73.7%	Pred. No. 1.1e-177		
Matches 1001: Conservative	0	Mismatches 331	Indels 27	Gaps 4

QY	1	ATGGCCCTCTCCACCGGTGCTGACCTGCTGCTGCCACTGGTGTCTCTGAGACGTGTTGGTG	60
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QY	61	GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTCACTCAGGGGACAGGAGAAAGA	120
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QY	121	GATTAGTGTGTGTCCCAAGGAAATATATCCACCTCAAAATTAATTGGATTTGCTGTACC	180
Db	365	GATTAATTTGTGTCCCAAGGAAAGATATGCCATCCAAAGAAATTAATTCATCTGCTGACCC	424
QY	181	AAGTCCCAAAAGAACCTACTTGTACATACATCTGCAGGCCCGGGGACAGATACGAC	240
Db	425	AAGTCCCAAAAGGAACCTACTTGTGTGATGTGATCTGTCCAAAGCCACAGGGACAGAAACATC	484
QY	241	TTCAGGAGATGTGAGAGCGGCTCTTTCACCGCTTCAGAAAAACCACTCAGACACTGCTC	300
Db	485	TTCGAGCTCTCTCATAAAGGACACTTTATACAGTCTTGCGAAGAACCACTCAGACACTGCTC	544
QY	301	AGCTCTCCAAATGCGCGAAGAAAGAAATGGGTAGGTGAGATCTTCTTTGACACGTGAC	360

Db 725 AAMCAGAACCCGCTGTGTAACGTGCCACGACGATTCTTTCTAAGCGGAAATGATGACACC 784
Oy 541 TCCCTGTAAGTAAGTAAAGAAAGCCCTGGAGTGCACAGATGTGCTACCCAGATTGAG 600
Db 785 CTTTGACACCACTGCAGAAATGATGAAGCTGTGCTACCTCCAGTTGCA 844
Oy 601 AATGTTAAGGCACTGAGACTCAGGACACAGTGTGTCCTGGTCAATTTCTTTT 660
Db 845 AATGTCACAAACCCCGAGACTCAGAGTACTGCGGCTGTGCCCTGTGTTATCTTCCTA 904
Oy 661 GGTCTTGGCTTTTATTCCTCTCTTCATTTGTTTAAATGATGCTACCAACGTTGAAG 720
Db 905 GGTCTTGGCTTTTATTCCTTTATCTGATCAGTCTACTGTGCCGATATCCCAAGTGAAG 964
Oy 721 TCCAGCTCTACTCCATGTGTTGTGGAAATGCACCTGAAAAAGAGGGAGCTTGA 780
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Oy 835 TTGACCCCGACCTGGGCTTACGTCGCTGCCAG-----TTCCACCTTC 879
Db 1085 TTCAACCCCACTGTGGCTTGACACACCCACGCTTCAGTCACTGTCTCCAGTACC 1144
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Db 1145 CCCATCAGCCCGCTGTGCTGCTAGTAACTGGCACAACTTCGTGTCACCTGTGAAGAG 1204
Oy 940 GTGACACACCCCTATCAGGGGGCTGACCCCACTTGGACACAGCCCTGCGCTCCGACCC 999
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Db 1262 ATCCCGCCCTGTTCGGAATGGGAAGACGTTCGCGGCCACGACCAACGGCTTGAC 1321
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Db 1322 ACTGAGAACCCCTGATGCTGTATGCTGTGGATGGCTGCTCGACACAGCTGGAAG 1381
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Db 1382 GAGTTCAATGCGCTCTCTGGGGCTGAGCGACGAGATCGAGCGTTGGAGCTGCAGAAC 1441
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Search completed: December 4, 2002, 20:15:47
Job time : 99 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:14:50 : Search time 265 Seconds
(Without alignments)
11625.410 Million cell updates/sec

Title: US-09-899-429A-1

Perfect score: 1368
Sequence: 1 atgggcctccacccgtgccc.....cgccagctcttcacagatga 1368

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

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- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1366.4	99.9	1368	14	AAO49932
2	1366.4	99.9	1368	21	AAO495105
3	1366.4	99.9	2088	12	AAO10883
4	1366.4	99.9	2088	12	AAO33946
5	1366.4	99.9	2111	20	AAO29170
6	1366.4	99.9	2111	22	AAO48859
7	1366.4	99.9	2111	24	ABK84039
8	1366.4	99.9	2111	24	ABN95862
9	1366.4	99.9	2161	21	AAZ48475

10	1366.4	99.9	2161	24	ABK13194	Human tumour necro
11	1364.8	99.8	2111	12	AAO10955	Encodes human 55kD
12	1364.8	99.8	2175	16	AAO90513	p55 TNF-R gene, H
13	1363.2	99.6	2062	13	AAO20973	TNF-alpha binding
14	1363.2	99.6	2062	13	AAO24440	Encodes TNF-alpha
15	1363.2	99.6	2176	12	AAO12215	Type I TNF receptor
16	1361.6	99.5	2141	11	AAO06285	Human Tumour Necro
17	1360	99.4	2170	14	AAO50870	p55 Tumour necrosl
18	1120.4	81.9	1334	11	AAO06282	Plasmodium Tumour Nec
19	743.4	54.3	2130	24	ABK63694	Rat sequence diffe
20	732.2	53.5	2173	11	AAO06284	Rat Tumour Necrosl
21	632.8	46.3	6926	18	AAO4431	Vector pCDNA3-1rg1
22	632.4	46.2	6889	17	AAO15931	DHFR/Intfcon (WTAS
23	596.8	43.6	608	13	AAO24441	Encodes truncated
24	515.4	37.7	1478	20	AAO58150	CadC-fusion polype
25	514	37.6	1301	18	AAO4022	CDNA for TBP(20-19
26	506	37.0	1147	18	AAO4021	CDNA for TBP(20-19
27	501.4	36.7	504	13	AAO24445	Encodes truncated
28	483	35.3	483	19	AAO1548	Human soluble tumo
29	483	35.3	483	19	AAO19801	Soluble tumour nec
30	483	35.3	483	20	AAO1732	Tumour necrosis in
31	483	35.3	483	22	AAO33945	Human 30 kDa TNF 1
32	440	32.2	2254	21	AAO55104	Partial human TNFR
33	424.4	31.0	1049	18	AAO94007	CDNA for TBP(20-16
34	424.4	31.0	1202	18	AAO94008	CDNA for TBP(20-16
35	418	30.6	1674	21	AAO50196	Male fusion plasml
36	381	27.9	1977	24	ABO59913	TNF-selectokline pr
37	376.2	27.5	477	13	AAO24444	Encodes truncated
38	375.8	27.5	507	24	ABO59490	Target canine gene
39	357.2	26.1	474	13	AAO24442	Encodes truncated
40	329.6	24.1	5870	21	AAO15044	Nucleotide sequenc
41	312.4	22.8	339	19	AAO19804	Truncated sTNFR, s
42	310.8	22.7	462	13	AAO24443	Encodes truncated
43	308.2	22.5	333	19	AAO19805	Truncated sTNFR, s
44	304.4	22.3	332	19	AAO19803	Truncated sTNFR, s
45	294.6	21.5	315	19	AAO19806	Truncated sTNFR, s

ALIGNMENTS

RESULT 1	AAO49932	standard; CDNA to mRNA; 1368 BP.
ID	AAO49932:	
AC	AAO49932:	
XX	29-APR-1994	(first entry)
XX	Lambda-derived	TNF-R CDNA.
XX	Human;	tumour necrosis factor receptor; TNF-R; Interleukin-1 receptor;
KW	IL-1R;	fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW	rheumatoid arthritis; diabetes;	multiple sclerosis; septic shock;
KW	pulmonary fibrosis; silicosis;	allotransplant; xenograft; rejection;
KW	graft versus host disease; sepsis;	inflammation; allergy;
KW	autoimmune dysfunction; ss.	
XX	Homo sapiens.	
OS	Lambda-gt10-7-ctnfp.	
XX	Key	Location/Qualifiers
FT	CD5	1..1366
FT	/*tag= a	/product= hTNF-R
FT	sig_peptide	1..120
FT	mat_peptide	/*tag= b
FT	121..1363	/*tag= c
XX	MO9319777-A.	
XX	14-Oct-1993.	

DE	Human TNFR1 coding sequence.
XX	TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW	tumour; cancer; apoptosis; bacterial infection; ds.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..1368
FT	/*tag= a
FT	/product= "TNFR1"
FT	1..39
FT	/*tag= b
FT	/number= 1
FT	replace(36,G)
FT	/*tag= c
FT	40..193
FT	/*tag= d
FT	/number= 2
FT	194..322
FT	/*tag= e
FT	/number= 3
FT	replace(224,T)
FT	/*tag= f
FT	replace(269,T)
FT	/*tag= g
FT	323..472
FT	/*tag= h
FT	/number= 4
FT	replace(362,A)
FT	/*tag= i
FT	replace(403,C)
FT	/*tag= j
FT	473..551
FT	/*tag= k
FT	/number= 5
FT	552..625
FT	/*tag= l
FT	/number= 6
FT	626..739
FT	/*tag= m
FT	/number= 7
FT	740..768
FT	/*tag= n
FT	/number= 8
FT	769..1057
FT	/*tag= o
FT	/number= 9
FT	1058..1368
FT	/*tag= p
FT	/number= 10
XX	
PN	WO200050436-A1.
XX	
PD	31-AUG-2000.
XX	
PE	23-FEB-2000; 2000WO-US04606.
XX	
PR	23-FEB-1999; 99US-0121314.
XX	
PA	(GENA-) GENAISSANCE PHARM INC.
PA	(NAND/) NANDABALAN K.
PA	(SCHU/) SCHULZ V P.
PA	(STEP/) STEPHENS J C.
PA	(CHEW/) CHEW A.
XX	
PI	Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX	
DR	WPI: 2000-543909/49.
DR	P-PSDB: AAB23446.
XX	
PT	Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the

[illegible]

Db 721 TCCAAAGCTTACTCCATTGTTTGGGAAATGCACACTGAAAAAGAGGGGAGCTTGAA 780
QY 781 GGAAGTACTACTAAGCCCGCCGCCCCAAACCAAGCTTACAGTCCACTCCAGGCTTAC 840
Db 781 GGAAGTACTACTAAGCCCGCCGCCCCAAACCAAGCTTACAGTCCACTCCAGGCTTAC 840
QY 841 CCCACCCCTGGGCTTCAGTCCGCTGCCCCAGTTCCACCTTACCTCCAGCTTAC 900
Db 841 CCCACCCCTGGGCTTCAGTCCGCTGCCCCAGTTCCACCTTACCTCCAGCTTAC 900
QY 901 CCGGATGAGTGTCCCAACTTGGGGCTCCCCGAGAGAGAGTGGCACCACCTTCAGAGG 960
Db 901 CCGGATGAGTGTCCCAACTTGGGGCTCCCCGAGAGAGTGGCACCACCTTCAGAGG 960
QY 961 GCTGACCCCATCTTCCGAGAGCCCTGCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1020
Db 961 GCTGACCCCATCTTCCGAGAGCCCTGCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1020
QY 1021 TGGGAGAGACAGCCGACCAAGCCACAGAGCTAGACACTGATGACCCCGGAGCTGTAC 1080
Db 1021 TGGGAGAGACAGCCGACCAAGCCACAGAGCTAGACACTGATGACCCCGGAGCTGTAC 1080
QY 1081 GCGGTGTGAGAGAACGTGCCCCCGTTCGCTGGAAGAAATTCGTGGGGGCTTACAGGCTG 1140
Db 1081 GCGGTGTGAGAGAACGTGCCCCCGTTCGCTGGAAGAAATTCGTGGGGGCTTACAGGCTG 1140
QY 1141 AGGACACAGAGATGATGAGTGGCTGAGTCTGCAGAACGGGGCTGCTGCGCGAGCGCAA 1200
Db 1141 AGGACACAGAGATGATGAGTGGCTGAGTCTGCAGAACGGGGCTGCTGCGCGAGCGCAA 1200
QY 1201 TACAGCATGCTGGCGAAGCTGAGAGGGCGGACGCGCGGGCGGAGGCGCAGCTGAGCTG 1260
Db 1201 TACAGCATGCTGGCGAAGCTGAGAGGGCGGACGCGCGGGCGGAGGCGCAGCTGAGCTG 1260
QY 1261 CTGGGAGCGGTGCTCCGCGAGATGAGACTGCTGGGGCTGCTGAGAGACATGAGAGGCG 1320
Db 1261 CTGGGAGCGGTGCTCCGCGAGATGAGACTGCTGGGGCTGCTGAGAGACATGAGAGGCG 1320
QY 1321 CTTTGGGGCGCCGCGCCCTCCCGCCGCGGCGCCAGTCTTCTCAGATGA 1368
Db 1321 CTTTGGGGCGCCGCGCCCTCCCGCCGCGGCGCCAGTCTTCTCAGATGA 1368
RESULT 3
AAQ10883
ID AAQ10883 standard; cDNA; 2088 BP.
XX
AC AAQ10883;
XX
DT 13-MAY-1991 (first entry)
XX
DE 30kD TNF inhibitor precursor gene in lambda-gt10-7ctnbp.
XX
KW Tumour necrosis factor; inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key CDS Location/Qualifiers
FT CDS 171..1536
FT /tag= a
XX
PN AU9058976-A.
PD 24-JAN-1991.
XX
PF 16-JUL-1990; 90AU-0058976.
XX
PR 07-FEB-1990; 90US-0479661.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
XX
PA (SYNE-) SYNERGEN INC.

DR WPI; 1991-073847/11.
DR P-PSDB; AAR10986.
XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
XX
XX Disclosure; Fig 21: 142bp; English.
XX
XX The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC prep. from RNA form U937 cells treated with PMA/PMA. The whole
CC gene can be inserted into expression vectors for prep. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also AAQ10878, AAQ10884 and AAQ10907.
XX
SQ Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
Query Match 99.9%; Score 1366.4; DB 12; Length 2088;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 169 ATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 228
QY 61 GGAATATACCCCTCAGGGGTTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 229 GGAATATACCCCTCAGGGGTTATTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 288
QY 121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCCTCAAAATATTCGATTGCTGTACC 180
Db 289 GATAGTGTGTGCTCCCAAGGAAATATATCCACCCTCAAAATATTCGATTGCTGTACC 348
QY 181 AATGGCAAAAGAAAGCACTTGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 349 AATGGCAAAAGAAAGCACTTGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 408
QY 241 TGCAGGAGAGTGTGAGAGCGGCTCTCACCGCTTCAGAAACACACCTCAGACACTGCTC 300
Db 409 TGCAGGAGAGTGTGAGAGCGGCTCTCACCGCTTCAGAAACACACCTCAGACACTGCTC 468
QY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360
Db 469 AGCTGCTCCAAATGCCGAAAGGAAATGGGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 528
QY 361 CGGAGACCGGTGTGTGGCTGAGAGAAACAGTACCGGATATGAGTGAAGAAACCTT 420
Db 529 CGGAGACCGGTGTGTGGCTGAGAGAAACAGTACCGGATATGAGTGAAGAAACCTT 588
QY 421 TTCCAGTGTTCATTTGACAGCCCTGCTCAATGGAGACCTGACCTCTCCTCCAGAG 480
Db 589 TTCCAGTGTTCATTTGACAGCCCTGCTCAATGGAGACCTGACCTCTCCTCCAGAG 648
QY 481 AAACAGAACACCGTGTGACACTGTCATGCAAGTTTCTTTCTAAGAGAAACGAGTGTGTC 540
Db 649 AAACAGAACACCGTGTGACACTGTCATGCAAGTTTCTTTCTAAGAGAAACGAGTGTGTC 708
QY 541 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 709 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
QY 601 AATGTTAAGGACAGTACAGACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 660
Db 769 AATGTTAAGGACAGTACAGACACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 828
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Db 829 GGTCTTTGCTTTTATCCCTCTCTTCAATGTTTATGATGATGATGATGATGATGATGATGATGAT 888
QY 721 TCCAGCTTACTCCATTTGTTGTGGGAAATGCACACCTGAAAAAGAGGGAGCTTGAA 780
Db 889 TCCAGCTTACTCCATTTGTTGTGGGAAATGCACACCTGAAAAAGAGGGAGCTTGAA 948

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Oy	841	CCCAACCTTGGGGCTTCAGTCCCGTGCACCAGTTCACACTTTCACCTCCAGCTCCACCTATACC	9000
Db	1009	CCCAACCTTGGGGCTTCAGTCCCGTGCACCAGTTCACACTTTCACCTCCAGCTCCACCTATACC	1060
Oy	901	CCCGGTACCTGTCCCAACTTTTGGGGCTTCCCGGCAGAGAGAGTGGGACCACTTATCAGGGG	9600
Db	1069	CCCGGTACCTGTCCCAACTTTTGGGGCTTCCCGGCAGAGAGAGTGGGACCACTTATCAGGGG	1120
Oy	961	GCTGACCCCATCTTGGCAGACGCCCTGCCTGCCACCCCATCCCAACCCCTTCAGAG	1020
Db	1129	GCTGACCCCATCTTGGCAGACGCCCTGCCTGCCACCCCATCCCAACCCCTTCAGAG	1180
Oy	1021	TGGGAGGACAGCGCCGACACAGCCACAGAGCCTAGACACTGATGACCCCGGACGCTGTAC	1080
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Db	1249	GCCGTGTGTGGAGAACGTGCTCCCGCTTGGGCTGTGAAGGAATTCGTGTGGGGCTTATGGGCTG	1300
Oy	1141	AGCGACCAAGAGATGATGATGGGCTGGAGCTGAGAAAGGAGGCGCTCTGTGGGAGGCGCAA	1200
Db	1309	AGCGACCAAGAGATGATGATGGGCTGGAGCTGAGAAAGGAGGCGCTCTGTGGGAGGCGCAA	1360
Oy	1201	TACAGCATGCTGTGGGACCTGTGAAGGCGGCGCAAGCGCGGCGCGAGGACAGCTTGGAGCTG	1260
Db	1369	TACAGCATGCTGTGGGACCTGTGAAGGCGGCGCAAGCGCGGCGCGAGGACAGCTTGGAGCTG	1420
Oy	1261	CTGGGACCGCTGTCTCCGGGACATGAGACTGCTGGGGCTTCCCTGTGAGGACATTCGAGGAGCGG	1320
Db	1429	CTGGGACCGCTGTCTCCGGGACATGAGACTGCTGGGGCTTCCCTGTGAGGACATTCGAGGAGCGG	1480
Oy	1321	CTTTTCGGGCGCCGCGCGGCGCTCCCGCGCGCGCCAGTCTTTCAGATGA	1368
Db	1489	CTTTTCGGGCGCCGCGCGGCGCTCCCGCGCGCGCCAGTCTTTCAGATGA	1536
RESULT 4			
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ID	AAC83946	standard; DNA; 2088 BP.	
xx	xx		
AC	AAC83946;		
xx	xx		
DT	02-MAR-2001 (first entry)		
xx	xx		
DE	Human 30 kDa TNF inhibitor precursor coding sequence.		
xx	xx		
KM	TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin.		
KW	IL-1; inflammatory disease; degenerative disease; human; ss.		
OS	Homo sapiens.		
xx	xx		
PN	US6143866-A.		
xx	xx		
PD	07-NOV-2000.		
xx	xx		
PF	19-JAN-1995;	95US-0375242.	
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PR	19-JUL-1990;	90US-0555274.	
PR	09-JUL-1993;	93US-0090366.	
PR	18-JUL-1989;	89US-0381080.	
PR	11-DEC-1989;	89US-0450329.	
PR	07-FEB-1990;	90US-0479661.	
xx	xx		
PA	(AMGE-) AMGEN INC.		
xx	xx		
PI	Squires C, King MW, Hale KK, Brewer MT, Thompson RC; Vanderlize RW, Vannice J, Kohno T;		

XX	WPI: 2001-006443/01.
DR	P-PSDB: AAB37677.
XX	
PT	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT	non-native cysteine residue cross-linked with polyethylene glycol,
PT	useful for treating inflammatory and degenerative diseases mediated by
PT	TNF -
XX	
PS	Example 6; Fig 21; 82pp; English.
XX	
CC	The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC	novel TNF inhibitors of the present invention are useful as therapeutic
CC	agents for inhibiting the activity of TNF and Interleukin (IL-1), and
CC	for treating inflammatory and degenerative diseases mediated by TNF. The
CC	present sequence is the coding sequence for the precursor of 30 kDa TNF
CC	inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX	
SQ	Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other:

Query Match	99.9%	Score 1366.4	DB 22	Length 2088
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1367	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

Qy	1	ATGGGCTCTCCACCGTCTGCTGACCTGGTGTGGCACTGGAGTGCATCGAGACCTTTGGTG	60
Db	169	ATGGGCTCTCCACCGTCTGACCTGCTGCTGGCGCTGGTGTCTCTGAGACTT7TG6TG	228
Qy	61	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAGA	120
Db	229	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGGACAGGGAGAGA	288
Qy	121	GATTACTGTGTGCCCCAAGGAAATATATCCACCCTCAAAATTAATTTGGATTGTGTACC	180
Db	289	GATTACTGTGTGCCCCAAGGAAATATATCCACCCTCAAAATTAATTTGGATTGTGTACC	348
Qy	181	AAAGTCCACAAAGAAACCTACTTGTACAACTACTGTCCAGGCCCGGGGACAGATACGGAC	240
Db	349	AAAGTCCACAAAGAAACCTACTTGTACAACTACTGTCCAGGCCCGGGGACAGATACGGAC	408
Qy	241	TTCGAGGAGATGTGAGAGGGGCTCTTTCACCCGCTTCAGAAAAACACTCAGACACTGGCTC	300
Db	409	TTCGAGGAGATGTGAGAGGGGCTCTTTCACCCGCTTCAGAAAAACACTCAGACACTGGCTC	468
Qy	301	AACTGCTCCAAATGCGCAAGAAAGAAATGGGTGAGGTGAGATCTTCTTTCGACAGTGGAC	360
Db	469	AACTGCTCCAAATGCGCAAGAAAGAAATGGGTGAGGTGAGATCTTCTTTCGACAGTGGAC	528
Qy	361	CGGGAACCCGTGTGTGGCTGCAGAGAAACCACTACGGGACTTATTGGAGTGAACCTT	420
Db	529	CGGGAACCCGTGTGTGGCTGCAGAGAAACCACTACGGGACTTATTGGAGTGAACCTT	588
Qy	421	TTTCAAGTGCTTCAATTTGAGGCTGTGCTCAATATGAGACCGTGCACCTCTCCCTGCCAGAG	480
Db	589	TTTCAAGTGCTTCAATTTGAGGCTGTGCTCAATATGAGACCGTGCACCTCTCCCTGCCAGAG	648
Qy	481	AAACAGAACACCGTGTGTCACCTGCCATCGACAGTTCCTTTCTAAGAGAAACGAGTGTGC	540
Db	649	AAACAGAACACCGTGTGTCACCTGCCATCGACAGTTCCTTTCTAAGAGAAACGAGTGTGC	708
Qy	541	TCCCTGAGTAACGTGAAGAAAAAGCTGGAGTGCAGAGAAAGTTGTGCTCAACCCCAATTGAG	600
Db	709	TCCCTGAGTAACGTGAAGAAAAAGCTGGAGTGCAGAGAAAGTTGTGCTCAACCCCAATTGAG	768
Qy	601	AAATGTTAAGGGCACTGAGAGACTCAGGACACACAGTGTGTTGCCCTGTCTATTTCTTT	660
Db	769	AAATGTTAAGGGCACTGAGAGACTCAGGACACACAGTGTGTTGCCCTGTCTATTTCTTT	828
Qy	661	GGTCTTTGGCTTTTATCCCTCCTCTCATTTGGTTAAATGATATGGCTACCAACGGTGGAG	720
Db	829	GGTCTTTGGCTTTTATCCCTCCTCTCATTTGGTTAAATGATATGGCTACCAACGGTGGAG	888


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Dh 667 AACAGAACACCGTGTGTCACCTGATGCAAGTTCTTTCTAAGAGAAAAGAGTGTGC 726
Oy 541 TCCGTGTAGTACTGTAGAAAAGCCGTGAGTGCAGAAAGTGTGCTTACCCCAATTGAG 600
Dh 727 TCCGTGTAGTACTGTAGAAAAGCCGTGAGTGCAGAAAGTGTGCTTACCCCAATTGAG 786
Oy 601 AATGTAAAGGACACTGAGAGACTCAGGCACACAGATGCTGTGCCCCGTGATTTCTTT 660
Dh 787 AATGTAAAGGACACTGAGAGACTCAGGCACACAGATGCTGTGCCCCGTGATTTCTTT 846
Oy 661 GGTCTTTGCCCCCTTTATCCCTCTCTCTCATGTTGTTTAAATGATGCTTACCAAGGTGAG 720
Dh 847 GGTCTTTGCCCCCTTTATCCCTCTCTCTCATGTTTAAATGATGCTTACCAAGGTGAG 906
Oy 721 TCCAAAGCTCTTCTCATTTGTTTGTGGAAAATGCACCTGAAAAGAGGGGAGCTTGAA 780
Dh 907 TCCAAAGCTCTTCTCATTTGTTTGTGGAAAATGCACCTGAAAAGAGGGGAGCTTGAA 966
Oy 781 GGAATCTACTAGTACCCCTGGCCCCCAAAACCAAGCTTCACTCCAGGCTTCAAC 840
Dh 967 GGAATCTACTAGTACCCCTGGCCCCCAAAACCAAGCTTCACTCCAGGCTTCAAC 1026
Oy 841 CCCACCCCTGGGCTTCACTCCGCTCCCAAGTTCACCTTCACTCCAGCTCAGCTATACC 900
Dh 1027 CCCACCCCTGGGCTTCACTCCGCTCCCAAGTTCACCTTCACTCCAGCTCAGCTATACC 1086
Oy 901 CCCGCTGACTCTCCCAACTTTGGGGCTCCCGCAGAGAGTGTGACCACTTATCAGGG 960
Dh 1087 CCCGCTGACTCTCCCAACTTTGGGGCTCCCGCAGAGAGTGTGACCACTTATCAGGG 1146
Oy 961 GCTGACCCCATCTTGGGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTACAGAG 1020
Dh 1147 GCTGACCCCATCTTGGGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTACAGAG 1206
Oy 1021 TGGAGAGACAGCCGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGAC 1080
Dh 1207 TGGAGAGACAGCCGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGAC 1266
Oy 1081 GCCCTGTGTGAGAACTGTCCCTGCTGTGGAAGAAATTCGTGCGGCTTACGGGCTG 1140
Dh 1267 GCCCTGTGTGAGAACTGTCCCTGCTGTGGAAGAAATTCGTGCGGCTTACGGGCTG 1326
Oy 1141 AGCAGCACAGAGATGATCGATCGGCTGAGAGTGCAGAAAGGGGCTCTCTGCGGAGGCGAA 1200
Dh 1327 AGCAGCACAGAGATGATCGATCGGCTGAGAGTGCAGAAAGGGGCTCTCTGCGGAGGCGAA 1386
Oy 1201 TACAGCATGCTGGCGACCTGAGAGCGCGGCGGCGGCGGAGGCCAGCTTGAAGCTG 1260
Dh 1387 TACAGCATGCTGGCGACCTGAGAGCGCGGCGGCGGCGGAGGCCAGCTTGAAGCTG 1446
Oy 1261 CTGGGAGCGGCTGCTCCGCGAATGAGACCTGCTGGGCTGCTGGAGGACATGAGAGAGCG 1320
Dh 1447 CTGGGAGCGGCTGCTCCGCGAATGAGACCTGCTGGGCTGCTGGAGGACATGAGAGAGCG 1506
Oy 1321 CTTTGGGCGCCCGCGGCTCTCCCGCGGCGGCGGCGGAGCTTCTCAGATGA 1368
Dh 1507 CTTTGGGCGCCCGCGGCTCTCCCGCGGCGGCGGCGGAGCTTCTCAGATGA 1554

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RESULT 6
AAH48859
ID AAH48859 standard; DNA; 2111 BP.
XX
AC AAH48859;
XX
XX 12-NOV-2001 (first entry)
DE Human TNFBP-associated DNA #1.
XX
XX TNF: tumor necrosis factor binding protein; TNFBP: treatment;
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotzoal; treatment; meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.

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XX OS Homo sapiens.
XX Key Location/Qualifiers
XX CDS 187..1554
XX FT /*tag= a
XX FT /product= "TNFBP-associated protein"
XX FT s1g-peptide 187..270
XX FT mat_peptide 271..1551
XX FT /*tag= b
XX FT /*tag= c
XX EP1132471-A2.
XX PD 12-SEP-2001.
XX PF 31-AUG-1990; 2001EP-0108117.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX PR 20-APR-1990; 90CH-0001347.
XX PR 31-AUG-1990; 90EP-0116707.
XX PR 31-AUG-1990; 99EP-0100703.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
XX PI Schlegel E;
XX WPI: 2001-559312/63.
XX P-PSDB: AAB86817.
XX PT New homogeneous, insoluble proteins that bind tumor necrosis factor
XX (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
XX PS Claim 4a; Fig 1; 26pp; German.
XX CC This invention describes novel insoluble proteins (i), also their
XX CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
XX CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
XX CC invention have antiinflammatory, immunosuppressive, antibacterial,
XX CC antiprotzoal activity. (i), and related recombinant proteins, are used
XX CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
XX CC sepsis; development of autoimmune glomerulonephritis and cerebral
XX CC malaria. Also (i), or antibodies specific for them, are used for
XX CC diagnostic determination of TNF in body fluids, for affinity purification
XX CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
XX CC human TNF binding protein described in the method of the invention.
SQ Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;
Query Match 99.98; Score 1366.4; DB 22; Length 2111;
Best Local Similarity 99.98; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ATGGGCGCTCCACAGCGCTGACCTGCTGCGACATGAGTGTGCTGGAGCTGTGGTG 60
Dh 187 ATGGGCGCTCCACAGCGCTGACCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 246
Oy 61 GGAATATACCCCTCAGGGGTATTGAGCTGTCCCTCACTAGGAGGAGAGAGAGA 120
Dh 247 GGAATATACCCCTCAGGGGTATTGAGCTGTCCCTCACTAGGAGGAGAGAGAGA 306
Oy 121 GATAGTGTGTCTCCCAAGAAAATATATTCACCTCAAAATTAATTCGATTGCTTACC 180
Dh 307 GATAGTGTGTCTCCCAAGAAAATATATTCACCTCAAAATTAATTCGATTGCTTACC 366
Oy 181 AAGTGCACAAGGAAGACCTACTTGTACAAATGACTGTCCAGGCGCGGGGACAGATACGAG 240
Dh 367 AAGTGCACAAGGAAGACCTACTTGTACAAATGACTGTCCAGGCGCGGGGACAGATACGAG 426
Oy 241 TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAAACCACTCAGACACTGCCTC 300
Dh 307 TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAAGAAAACCACTCAGACACTGCCTC

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D	427	TTGAGGGAGTGTGAGACGGGCTCTTACACGGTTCAGAAAACACCTCAGACATGCGTTC	486
Q	301	AGCTGCTCCAAATATGCGGAAAGAAATATGGCTCAGGTGAGATCTCTTCTTGCACTAGTGAC	360
D	487	AGCGCTCCAAATATGCGGAAAGAAATATGGCTCAGGTGAGATCTCTTCTTGCACTAGTGAC	546
Q	361	CGGAGACCGGTGTGGCTCAGGAAAGAACATACCGGATATATGAGTGAATAAACCCTT	420
D	547	CGGAGACCGGTGTGGCTCAGGAAAGAACATACCGGATATATGAGTGAATAAACCCTT	606
Q	421	TTCCAGTCTTCAATTTGACGCTCTGCTCTAAAGGAGACCGTGACCTCTCTGCGCAGAG	480
D	607	TTCCAGTCTTCAATTTGACGCTCTGCTCTAAAGGAGACCGTGACCTCTCTGCGCAGAG	666
Q	481	AAACAGAACACCGTGTGACCTGCATGCAAGTTCCTTCTTAAGAGAAAAGATGTGTG	540
D	667	AAACAGAACACCGTGTGACCTGCATGCAAGTTCCTTCTTAAGAGAAAAGATGTGTG	726
Q	541	TTCTGTAGTAACTGTAAAGAAAACCTGAGATGCACAGTTTGTGCTTACCCAGATTGAG	600
D	727	TTCTGTAGTAACTGTAAAGAAAACCTGAGATGCACAGTTCCTTCTTAAGAGAAAAGATGTG	786
Q	601	AATTTTAAGGGACACTGAGACTAGGACACACAGTCTGTGTGCCCCCTGCTCAATTTCTT	660
D	787	AATTTTAAGGGACACTGAGACTAGGACACACAGTCTGTGTGCCCCCTGCTCAATTTCTT	846
Q	661	GGCTTTGCTTTTATATCCCTCTTCAATTTGTTTAAATGATATGCTTACCAAGGTGGAAG	720
D	847	GGCTTTGCTTTTATATCCCTCTTCAATTTGTTTAAATGATATGCTTACCAAGGTGGAAG	906
Q	721	TTCAAGCTTACTCTCATTTGTTTGTGGGAAATGACACCTGAAAAAGAGGGGAGCTTGA	780
D	907	TTCAAGCTTACTCTCATTTGTTTGTGGGAAATGACACCTGAAAAAGAGGGGAGCTTGA	966
Q	781	GGAACTACTTCTAAAGCCCCGGGCCCCAAACCCAAAGTTAGTCCCACTCAGGCTTACAC	840
D	967	GGAACTACTTCTAAAGCCCCGGGCCCCAAACCCAAAGTTAGTCCCACTCAGGCTTACAC	1022
Q	841	CCCACTCTGGGGCTTCAAGTCCCGTGGCCAGTTCACCTTCACTCCAGCTCACTATAC	900
D	1027	CCCACTCTGGGGCTTCAAGTCCCGTGGCCAGTTCACCTTCACTCCAGCTCACTATAC	1088
Q	901	CCCGGTACTGTCCCAACTTTGGGGCTCCCCGACAGAGGTGGACACCTATACGGGG	960
D	1087	CCCGGTACTGTCCCAACTTTGGGGCTCCCCGACAGAGGTGGACACCTATACGGGG	1144
Q	961	GCTTACCCCACTTGGGAGAGGCGTCCGCTCCGACCCCATCCCAACCCCTTCAAG	1022
D	1147	GCTTACCCCACTTGGGAGAGGCGTCCGCTCCGACCCCATCCCAACCCCTTCAAG	1206
Q	1021	TGGAGAGACAGCGGCCCAAGCCACAGAGCTTAACTATGATGACCCCGACGCTGTAC	1080
D	1207	TGGAGAGACAGCGGCCCAAGCCACAGAGCTTAACTATGATGACCCCGACGCTGTAC	1266
Q	1081	GGCGTGTGAGAAAGTGGCCCCCGTTGGCTGAGAGAAATGTGTGCGGCTTACGGCTG	1144
D	1267	GGCGTGTGAGAAAGTGGCCCCCGTTGGCTGAGAGAAATGTGTGCGGCTTACGGCTG	1322
Q	1141	AGGCACACAGATCATTTGGGCTGGAGAGTGCACAAAGGGCGCTGCTGTGGAGAGCGCAA	1200
D	1327	AGGCACACAGATCATTTGGGCTGGAGAGTGCACAAAGGGCGCTGCTGTGGAGAGCGCAA	1386
Q	1201	TACAGCATGTGTGAGCACTTGAAGGCGGACACCGCGCGGAGGACACGCTGAGAGTG	1266
D	1387	TACAGCATGTGTGAGCACTTGAAGGCGGACACCGCGCGGAGGACACGCTGAGAGTG	1444
Q	1261	CTGGGACGCTGTCTCGCGCATGGAATGTGTGGCTGTCTTGAAGACATTCGAGAGAGCG	1320
D	1447	CTGGGACGCTGTCTCGCGCATGGAATGTGTGGCTGTCTTGAAGACATTCGAGAGAGCG	1506
Q	1321	CTTTTGGGGCCCCGCGCTTCCGCGCCCGGCGCCAGTCTTCTCAATGA 1368	
D	1507	CTTTTGGGGCCCCGCGCTTCCGCGCCCGGCGCCAGTCTTCTCAATGA 1554	

RESULT 7
ABR84039
ID ABR84039 standard; cDNA: 2111 BP.
XX ABR84039;
AC
XX
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #610.
XX
XX
KW Human; ss: granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
XX Homo sapiens.
OS
XX
XX WO200228999-A2.
PN
XX
XX 11-APR-2002.
PD
XX
XX 03-OCT-2001; 2001WO-US30821.
PF
XX
XX 03-OCT-2000; 2000US-237189P.
PR
XX
XX (GENE-) GENE LOGIC INC.
PA
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
XX WPI; 2002-435326/A6.
DR
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX
PS Claim 1; SEQ ID NO 610; 114pp; English.

CC Parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://ipo.int/pub/published_pcl_sequences/.

XX Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 99.9%; Score 1366.4; DB 24; Length 2111;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 ATGGGCGCTCTCCACCGCTGACTGCTGCTGCGCCACCTGCTGCTCTCTGAGCTGTTGGG 60
Db 187 ATGGGCGCTCTCCACCGCTGACTGCTGCTGCGCCACCTGCTGCTCTCTGAGCTGTTGGG 246
Oy 61 GGAATATACCCCTCAGGGGTTATTGAGCTGTCCTTCACCTAGGGGACAGGAGAAGA 120
Db 247 GGAATATACCCCTCAGGGGTTATTGAGCTGTCCTTCACCTAGGGGACAGGAGAAGA 306
Oy 121 GATAGTGTGTGTCCTCCAGGAATAATATATCCACCTCAAAATATTCGATTTGCTGTACC 180
Db 307 GATAGTGTGTGTCCTCCAGGAATAATATATCCACCTCAAAATATTCGATTTGCTGTACC 366
Oy 181 AAGTCCCAAGAAGAACCTTCTTGTACATGACTGTCCAGGCGCGGGGAGAGATACGAGAC 240
Db 367 AAGTCCCAAGAAGAACCTTCTTGTACATGACTGTCCAGGCGCGGGGAGAGATACGAGAC 426
Oy 241 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACTCAGACATGCGCTC 300
Db 427 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACACACTCAGACATGCGCTC 486
Oy 301 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGTCTTTGTCACAGTGGAC 360
Db 487 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGTCTTTGTCACAGTGGAC 546
Oy 361 CGGGACACCGTGTGGCTGCGAGAAACCACTACCGGCAATATTGGATGAAACCTT 420
Db 547 CGGGACACCGTGTGGCTGCGAGAAACCACTACCGGCAATATTGGATGAAACCTT 606
Oy 421 TTCCAGTGTCTCAATTTGACGCTCTGCGCTCAATGGGACCGTCTCTCTGCGCAGAG 480
Db 607 TTCCAGTGTCTCAATTTGACGCTCTGCGCTCAATGGGACCGTCTCTCTGCGCAGAG 666
Oy 481 AAACAGAACCGGTGTGACCTGTCATGCAAGGTTTCTTTCTAAGAGAAAAAGATGTGTTC 540
Db 667 AAACAGAACCGGTGTGACCTGTCATGCAAGGTTTCTTTCTAAGAGAAAAAGATGTGTTC 726
Oy 541 TCCCTGTAGTAAGTGTAAAGAAAGCCTGGAGTGCAGAAATTTGCTTACCCAGATGAG 600
Db 727 TCCCTGTAGTAAGTGTAAAGAAAGCCTGGAGTGCAGAAATTTGCTTACCCAGATGAG 786
Oy 601 AATGTTAAGGCACTGAGAGACTCAGGACACACAGTGTCTTCCCTGGTCAATTTCTTT 660
Db 787 AATGTTAAGGCACTGAGAGACTCAGGACACACAGTGTCTTCCCTGGTCAATTTCTTT 846
Oy 661 GGTCTTTGCTTTTATCCCTCTCTCATTTGATTTAATGCTTACCAACGGTGAAG 720
Db 847 GGTCTTTGCTTTTATCCCTCTCTCATTTGATTTAATGCTTACCAACGGTGAAG 906
Oy 721 TCCAAAGCTTACTCATTTTGTGGGAAATGACACCTGGAAGAAAGAGGGAGCTTGA 780
Db 907 TCCAAAGCTTACTCATTTTGTGGGAAATGACACCTGGAAGAAAGAGGGAGCTTGA 966
Oy 781 GGAATCTACTAGAGCCCTGGCCCAAAACCAAGCTTGTAGTCCCACTCAGAGCTTAC 840
Db 967 GGAATCTACTAGAGCCCTGGCCCAAAACCAAGCTTGTAGTCCCACTCAGAGCTTAC 1026
Oy 841 CCCACCTGGGCTTCAAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTCCACTATACC 900
Db 1027 CCCACCTGGGCTTCAAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTCCACTATACC 1086

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Oy 901 CCCGTGACTGTGCCACTTTGGGCTCCCGCAGAGAGGTGGACACCACTATCAGGG 960
Db 1087 CCCGTGACTGTGCCACTTTGGGCTCCCGCAGAGAGGTGGACACCACTATCAGGG 1146
Oy 961 GCTGACCCCATCTTTGCGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
Db 1147 GCTGACCCCATCTTTGCGACAGCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAG 1206
Oy 1021 TGGGAGACAGCGCCCAACAGCCAGACCTAGACATGATGATACCCCGACGCTGTAC 1080
Db 1207 TGGGAGACAGCGCCCAACAGCCAGACCTAGACATGATGATACCCCGACGCTGTAC 1266
Oy 1081 GCCGTGTGGAGAACGTGCCCCGTTGGGCTGGAAGGAATTCGTGCGGCGCTTAGGGCT 1140
Db 1267 GCCGTGTGGAGAACGTGCCCCGTTGGGCTGGAAGGAATTCGTGCGGCGCTTAGGGCT 1326
Oy 1141 AGCGACACAGAGATGATCGCTGAGCTGTGAGAACGGGCGCTGCTGCGGAGCGCAA 1200
Db 1327 AGCGACACAGAGATGATCGCTGAGCTGTGAGAACGGGCGCTGCTGCGGAGCGCAA 1386
Oy 1201 TACAGCATGTGTGGCACTGTGAGCGGCGCACGCGCGGCGGAGCCACGCTGAGCTG 1260
Db 1387 TACAGCATGTGTGGCACTGTGAGCGGCGCACGCGCGGCGGAGCCACGCTGAGCTG 1446
Oy 1261 CTGGAGCGGTGCTCCGAGCATGTGACCTGCTGAGGCTGCTGAGAGACATCGAGAGCG 1320
Db 1447 CTGGAGCGGTGCTCCGAGCATGTGACCTGCTGAGGCTGCTGAGAGACATCGAGAGCG 1506
Oy 1321 CTTTCCGGGCGCGCGCCCTCCCGCGCGCCAGCTTCTTCAGATGA 1368
Db 1507 CTTTCCGGGCGCGCGCCCTCCCGCGCGCCAGCTTCTTCAGATGA 1554

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RESULT 8
 ABN95862
 ID ABN95862 standard; DNA: 2111 BP.
 XX
 AC ABN95862;
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #2360 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 PE 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 XX
 DR WPI: 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 XX
 PS Claim 1: SEQ ID NO 2360; 298bp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver


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XX Key Location/Qualifiers
FH sig_peptide 187..273
FT /*tag-a
FT mat_peptide 274..1551
FT /*tag-b
FT /product= 55kd TNF-BP
XX
XX EP417563-A.
XX
XX 20-MAR-1991.
XX
XX 31-AUG-1990; 90BP-0116707.
XX
XX 20-APR-1990; 90CH-0001347.
XX 12-SEP-1989; 89CH-0003319.
XX 08-MAR-1990; 90CH-0000746.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
XX Schlaefer EJ;
XX WPI, 1991-081851/12.
XX P-PSDB; AAR11082.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
XX encoding them, useful in pharmaceutical prods. and for antibody
XX prodn.
XX
XX Claim 4; Fig 1; 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75kd
XX TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were
XX synthesised based on these partial sequences. The primers were
XX used to produce a cDNA fragment for use as a probe to screen a human
XX placental cDNA bank constructed in lambda gfil1. Positive clones were
XX identified and sequenced. DNA constructs comprising the TNF-BP coding
XX sequence may also contain a fragment encoding a human Ig domain.
XX Recombinant constructs are used to transform cells to confer
XX improved TNF-binding properties.
XX See also AA010956.
XX
XX Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other:
XX
XX Query Match 99.8%; Score 1364.8; DB 12; Length 2111;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 1366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ATGGGGCTCTCCACCGTGTGCTGACGTCGTCGCCACCTGCTGCTGAGCTGTGGTG 60
XX 187 ATGGGGCTCTCCACCGTGTGCTGACGTCGTCGCCCTGCTGCTGAGCTGTGGTG 246
XX
XX 61 GGAATATACCCCTCAGAGGGTATTGAGACTGTCCTCACCCTAGAGGAGACAGAGAGA 120
XX 247 GGAATATACCCCTCAGAGGGTATTGAGACTGTCCTCACCCTAGAGGAGACAGAGAGA 306
XX
XX 121 GATAGTGTGTGCCCAAGAGAAATATATCACACCTCAAAATTAATTCGATTGCTGTACC 180
XX 307 GATAGTGTGTGCCCAAGAGAAATATATCACACCTCAAAATTAATTCGATTGCTGTACC 366
XX
XX 181 AAGTGCACAAAGGAACCTACTTGTACATGACTGTCCAGGGCCGGGGGAGAGATTAGGAC 240
XX 367 AAGTGCACAAAGGAACCTACTTGTACATGACTGTCCAGGGCCGGGGGAGAGATTAGGAC 426
XX
XX 241 TGCAGAGAGTGTGAGAGCGGCTCTTACCGGCTTCAGAAACACCTCAGACACTGCTC 300
XX 427 TGCAGAGAGTGTGAGAGCGGCTCTTACCGGCTTCAGAAACACCTCAGACACTGCTC 486
XX
XX 301 AGCTGCTCCAATGCGGAAAGAAATGGTCAAGGTGAGAGATCTTCTTGACAGTGGAC 360
XX 487 AGCTGCTCCAATGCGGAAAGAAATGGTCAAGGTGAGAGATCTTCTTGACAGTGGAC 546
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QY 361 CGGACACCGGTGTGGTGTGACAGAGAAACAGTACCGGCAATTATTGAGTGAACCTT 420
DB 547 CGGACACCGGTGTGGTGTGACAGAGAAACAGTACCGGCAATTATTGAGTGAACCTT 606
QY 421 TTCCAGTGTCTCAATTTGACAGCTCTGCTCAATTTGAGACCGTGTGACAGGAG 480
DB 607 TTCCAGTGTCTCAATTTGACAGCTCTGCTCAATTTGAGACCGTGTGACAGGAG 666
QY 481 AAACAGAACACCGGTGTGACAGCTCTGCTCAATTTGAGACCGTGTGACAGGAG 540
DB 667 AAACAGAACACCGGTGTGACAGCTCTGCTCAATTTGAGACCGTGTGACAGGAG 726
QY 541 TCCGTGAGTACCTGTAAGAAAGCCGAGTGCAGCAAGTGTGAGTGTGAGTGTGAG 600
DB 727 TCCGTGAGTACCTGTAAGAAAGCCGAGTGCAGCAAGTGTGAGTGTGAGTGTGAG 786
QY 601 AATGTTAAGGACACGAGGACTGACAGCACAGTGTGAGTGTGAGTGTGAGTGTGAG 660
DB 787 AATGTTAAGGACACGAGGACTGACAGCACAGTGTGAGTGTGAGTGTGAGTGTGAG 846
QY 661 GGTCTTGTGCTTTTATCCCTCTTCAATTTGAGTGTGAGTGTGAGTGTGAGTGTGAG 720
DB 847 GGTCTTGTGCTTTTATCCCTCTTCAATTTGAGTGTGAGTGTGAGTGTGAGTGTGAG 906
QY 721 TCCAGCTCTACCTCCATTTGTTGTGGAAATGACACCTGAAAGAGAGGGGAGTGA 780
DB 907 TCCAGCTCTACCTCCATTTGTTGTGGAAATGACACCTGAAAGAGAGGGGAGTGA 966
QY 781 GGAACCTACTACTAAGCCCTGAGCCCAACCCAGCTTCACTCCAGGCTTCAAC 840
DB 967 GGAACCTACTACTAAGCCCTGAGCCCAACCCAGCTTCACTCCAGGCTTCAAC 1026
QY 841 CCCACCTCTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 1027 CCCACCTCTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1086
QY 901 CCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1087 CCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 961 GCTGACCCCATCTTGTGACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 1147 GCTGACCCCATCTTGTGACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1206
QY 1021 TGGGAGGACAGGCGCCACAGCCACAGAGCTTACACTGATGATGATGATGATGATGATGAT 1080
DB 1207 TGGGAGGACAGGCGCCACAGCCACAGAGCTTACACTGATGATGATGATGATGATGATGAT 1266
QY 1081 GCGGTGTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1267 GCGGTGTGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
QY 1141 AAGGACACAGAGTGTGATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
DB 1327 AAGGACACAGAGTGTGATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1386
QY 1201 TACAGCATCTGTGCGACCTGAGAGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
DB 1387 TACAGCATCTGTGCGACCTGAGAGCGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1446
QY 1261 CTGGGAGCGGTGCTGCGGACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1447 CTGGGAGCGGTGCTGCGGACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
QY 1321 CTTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1507 CTTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554
```

```
RESULT 12
AA090513
ID AA090513 standard; DNA; 2175 BP.
XX
```

AC	AA090513;	
XX		
DT	19-JAN-1996	(first entry)
XX		
DE	p55 TNF-R gene.	
XX		
KW	p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;	
KW	epidermal growth factor receptor; EGF-R; protease; inhibitor;	
KM	phorbol myristate acetate; PMA; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	location/Qualifiers
FT	CDS	256..1623
FT		/*tag= a
FT		/product= p55 TNF-R
FT	misc_signal	2143..2149
FT		/*tag= b
FT		/note= "possible poly-A signal"
XX		
PN	AU9475742-A.	
XX		
PD	04-MAY-1995.	
XX		
PE	11-OCT-1994;	94AU-0075742.
XX		
PR	12-OCT-1993;	93IL-0107268.
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Batkin M, Brakebusch C, Varfolomeev E, Wallach D;	
XX		
DR	WPI; 1995-194342/26.	
XX	P-PSDB; AAR75084.	
PT	New protease capable of cleaving soluble tumour necrosis factor	
PT	(TNF) receptor from cell-bound TNF-receptor, useful for	
PT	antagonising deleterious effects of TNF.	
XX		
PS	Disclosure: Fig 1; 40pp; English.	
XX		
CC	This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.	
CC	Expression of this receptor is regulated by shedding of the	
CC	extracellular receptor fragment. The p55 TNF-R can be shed in response	
CC	to different inducing agents, e.g. phorbol myristate acetate (PMA),	
CC	depending on cell type. The only region of the receptor whose structure	
CC	affects the shedding response is the spacer region (see AAR75012) in the	
CC	extracellular domain. This region is located close to a site of cleavage	
CC	of the molecule, and links the Cys rich module to the transmembrane	
CC	domain. The spacer region of the encoded protein was used to create the	
CC	chimeras between human p55 TNF-R and murine epidermal growth factor	
CC	receptor (EGF-R) that are represented by AAR75007-11. This spacer region	
CC	was subjected to deletion mutations (AAR75013-25) and substitutions	
CC	(AAR75026-47). Of the spacer region, the most important residues are	
CC	Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most	
CC	important of these. The shedding of the receptor is independent of the	
CC	side chain identity of these residues, with the exception of a limited	
CC	dependence on the identity of Val 173. Mutations which alter the	
CC	conformation of the protein adversely effect the shedding process. The	
CC	mutations shown in AAR75013-47 were introduced in order to create an	
CC	inhibitor of a protease that is capable of cleaving the soluble TNF-R	
CC	from the cell bound TNF-R. Fragments of these inhibitors can be seen in	
CC	AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease	
CC	inhibitors can be used for enhancing TNF function.	
XX		
SO	Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;	
Query Match	99.8%;	Score 1364.8; DB 16; Length 2175;
Best Local Similarity	99.9%;	Pred. No. 0;
Matches 1366;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0

1 ATGGGCTCTCCACCGTGGCTGACCTGCTGTCGACCACTGCTGCTCTGAGAGCTGTGGTG 60

|||||

[illegible]


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QY 961 GCTGACCCCATCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
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Db 1115 GCTGACCCCATCTTGGCAGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1174
QY 1021 TGGGAGGACAGCGCCCAACAGCCACAGAGCTAGACATGTATGACCCCGCAGCTGTAC 1080
    |||
Db 1175 TGGGAGGACAGCGCCCAACAGCCACAGAGCTAGACATGTATGACCCCGCAGCTGTAC 1234
QY 1081 GCCGTGTGTGAGAAAGTCCCGCTTGGCGCTGGAAGAATTGTCGGCGCTAGAGCTG 1140
    |||
Db 1235 GCCGTGTGTGAGAAAGTCCCGCTTGGCGCTGGAAGAATTGTCGGCGCTAGAGCTG 1294
QY 1141 AGCGACACGAGATGATGCTGGCTGGAGCTGCAGAAAGCGGCGCTGCTCGCGAGCGCAA 1200
    |||
Db 1295 AGCGACACGAGATGATGCTGGCTGGAGCTGCAGAAAGCGGCGCTGCTCGCGAGCGCAA 1354
QY 1201 TACAGCATGCTGGGAGCACTGAGAGCGGCGCACCGCGCGCGAGGCCACCTGAGACTG 1260
    |||
Db 1355 TACAGCATGCTGGGAGCACTGAGAGCGGCGCACCGCGCGCGAGGCCACCTGAGACTG 1414
QY 1261 CTGGGACGCGTGTCTCCGCGACATGAGACTGCTGGGCTGCTGGAGGACATGAGAGGCG 1320
    |||
Db 1415 CTGGGACGCGTGTCTCCGCGACATGAGACTGCTGGGCTGCTGGAGGACATGAGAGGCG 1474
QY 1321 CTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
    |||
Db 1475 CTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522
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RESULT 14

AAQ24440

ID AAQ24440 standard; DNA: 2062 BP.

XX AC AAQ24440;

DT 05-NOV-1992 (first entry)

XX DE Encodes TNF-alpha 55kd receptor.

XX KM tumour necrosis factor alpha: extracellular binding domain;

XX KM treatment: pulmonary diseases; septic shock; HIV infection; AIDS;

XX KM malaria; viral meningitis; graft versus host disease;

XX KM autoimmune disease; rheumatoid arthritis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FH CDS 156..1517

FT /*tag= a

FT /product= human TNF-alpha

FT mat_peptide 1265..1267

FT /*tag= b

FT /note= "3"

FT mat_peptide 1265..1267

FT /*tag= c

FT /codon= seq: "TGG", aa: Thr

FT mat_peptide 1258..1260

FT /*tag= d

FT /codon= Seq "AAG", aa: Leu

FT mat_peptide 1433..1435

FT /*tag= e

FT /codon= Seq: "GAC", aa: Asn

FT sig_peptide 156..274

XX /*tag= f

XX WO9207076-A.

XX 30-APR-1992.

XX 18-OCT-1991.

XX 91MO-GB01826.

XX 18-OCT-1990.

XX 90GB-0022648.

```
XX (CHAR-) CHARING CROSS SUNLEY RES CENT.
PA Brennan FM, Feldmann M, Gray PM, Turner MJC:
PI WPI: 1992-167156/20.
XX P-PSDB: AAR24000.
DR New polypeptide capable of binding human TNF alpha - comprises
XX first three cysteine-rich subdomains of TNF alpha receptor for
XX treating autoimmune disease, septic shock, HIV etc.
PS Claim 4: Fig 1: 43pp: English.
XX This sequence encodes human TNF-alpha 55kd receptor . A placenta cDNA
XX library in gl10 was screened with probe AAQ29236. Ten hybridising clones
XX were plaque purified and cDNA size determined by PAGE against an
XX Eco RI digested phage DNA. The inserts of two cDNA clones were then
XX sequenced. The coding region of the majority of the human TNF-alpha
XX 55kd receptor was isolated as an EcoRI fragment encoding 374 amino
XX acids, and cloned into a mammalian cell expression vector, resulting
XX in pTNFR. A derivative of the TNF-alpha receptor was produced by
XX engineering a termination codon just prior to the transmembrane
XX domain. PCR with primers AAQ29237,8 generated a 300bp
XX restriction fragment which was cloned into pTNFR, giving pTNFRcd.
XX CC DNA sequencing confirmed this contained the designed DNA sequence.
XX CC The TNF-alpha receptor expression plasmids were then transfected
XX CC into monkey COS-7 cells.
XX CC See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX S0 Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;
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Query Match 99.6%; Score 1363.2; DB 13; Length 2062;

Best Local Similarity 99.8%; Pred No. 0;

Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ATGGGCGCTCTCCACCGTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 155 ATGGGCGCTCTCCACCGTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
QY 61 GGAATATACCCCTCAGGGGTTATTGACTGTCTCTACCTAGAGGACAGGAGAAAGAGA 120
Db 215 GGAATATACCCCTCAGGGGTTATTGACTGTCTCTACCTAGAGGACAGGAGAAAGAGA 274
QY 121 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTGCTGTAC 180
Db 275 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATATGATTGCTGTAC 334
QY 241 TGCAGGAGTGTGAGACGGCTCTTCAACGCTTCAGAAAAACACCTCAGACATGCTC 300
Db 395 TGCAGGAGTGTGAGACGGCTCTTCAACGCTTCAGAAAAACACCTCAGACATGCTC 454
QY 301 AGTGTCTCCAAATCCGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 455 AGTGTCTCCAAATCCGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 514
QY 455 AGTGTCTCCAAATCCGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATG 574
Db 515 CGGAGACACCGTGTGCTGAGAGAAACAGATGATGATGATGATGATGATGATGATGATG 634
QY 421 TTCCAGTCTTCAATTGACAGCTCTGCTCAATGGACCGTGCACCTCTCTGACAGAG 480
Db 575 TTCCAGTCTTCAATTGACAGCTCTGCTCAATGGACCGTGCACCTCTCTGACAGAG 634
QY 481 AAACAGAAACCGGTGACACTGACATGACATGACATGACATGACATGACATGACATGAC 540
Db 635 AAACAGAAACCGGTGACACTGACATGACATGACATGACATGACATGACATGACATGAC 694
QY 541 TCTGTAGTAAGTAAGAAAGCGCTGAGTGCAGAGTGTGCTTACCCAGATTGAG 600
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|||||
Db 695 TCCTAGTACTGTAAGAAAAGCTGGAGTGCACAGAAATTGCTACCCAGATTGAG 754
Oy 601 AATGTAAAGGAGACGAGAGACTCAGACCAACAGATGCTGTCCCTGGTCAATTTCTTT 660
Db 755 AATGTAAAGGAGACGAGAGACTCAGACCAACAGATGCTGTCCCTGGTCAATTTCTTT 814
Oy 661 GGTCTTTGCTCTTTATCCCTCTCTTCATGTTTAAATGATGCTACCAAGGTGAAG 720
Db 815 GGTCTTTGCTCTTTATCCCTCTCTTCATGTTTAAATGATGCTACCAAGGTGAAG 874
Oy 721 TCCAAGCTCTACTCCATGTTTGTGGAAATGACACCTGAAAAAGAGGGAGCTTGA 780
Db 875 TCCAAGCTCTACTCCATGTTTGTGGAAATGACACCTGAAAAAGAGGGAGCTTGA 934
Oy 781 GGAATCTACTACTAACCCCTGGCCCCCAAAACCAAGCTTACGTCACCTCAGCTTCAAC 840
Db 935 GGAATCTACTACTAACCCCTGGCCCCCAAAACCAAGCTTACGTCACCTCAGCTTCAAC 994
Oy 841 CCCACCTGGGCTTGAATCCCTGCGCCAGTTCCACCTTCCAGCTCCACCTATACC 900
Db 995 CCCACCTGGGCTTGAATCCCTGCGCCAGTTCCACCTTCCAGCTCCACCTATACC 1054
Oy 901 CCCGCTGACTGTCCCAACTTTTGGCGCTCCCGCAGAGAGGTGGACACACCTATCAGGG 960
Db 1055 CCCGCTGACTGTCCCAACTTTTGGCGCTCCCGCAGAGAGGTGGACACACCTATCAGGG 1114
Oy 961 GCTGACCCCATCTCTTGCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAA 1020
Db 1115 GCTGACCCCATCTCTTGCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAA 1174
Oy 1021 TGGAGAGACAGCCGACACAGCCAGAGCCTAGACACTGATGACCCCGCGAGCGTAC 1080
Db 1175 TGGAGAGACAGCCGACACAGCCAGAGCCTAGACACTGATGACCCCGCGAGCGTAC 1234
Oy 1081 GCCGTGTGTGAGAGACGTGCCCCCGTGGCGCTGGAAGGAATTCGTGCGGCGCTAGGGCTG 1140
Db 1235 GCCGTGTGTGAGAGACGTGCCCCCGTGGCGCTGGAAGGAATTCGTGCGGCGCTAGGGCTG 1294
Oy 1141 AGCGACACAGAGATGATGCTGGCTGCAAGCTGCAAAAGGGCGCTGCTGCGCAGCGCA 1200
Db 1295 AGCGACACAGAGATGATGCTGGCTGCAAGCTGCAAAAGGGCGCTGCTGCGCAGCGCA 1354
Oy 1201 TACAGCATGTGGCGACCTGAGAGCGGCGCAGCGCGCGGCGAGGCGCAGCTGAGAGCTG 1260
Db 1355 TACAGCATGTGGCGACCTGAGAGCGGCGCAGCGCGCGGCGAGGCGCAGCTGAGAGCTG 1414
Oy 1261 CTGGGACGCGTCTCGCGACATGAGACCTGCTGGCTGCTGAGAGACATCGAGAGGCG 1320
Db 1415 CTGGGACGCGTCTCGCGACATGAGACCTGCTGGCTGCTGAGAGACATCGAGAGGCG 1474
Oy 1321 CTTTGGCGGCGCGCGCGCTCCCGCGCGCGCGCGCGCTTCTCAGATGA 1368
Db 1475 CTTTGGCGGCGCGCGCGCTCCCGCGCGCGCGCGCGCTTCTCAGATGA 1522

```

RESULT 15

AAQ12215 standard: DNA: 2176 BP.

AAQ12215;

DT 12-SEP-1991 (first entry)

DE Type I TNF receptor.

KW Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT terminator 244..246 /*tag= a

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FT CDS /note= "in-frame termination codon"
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FT FT /*tag= a
FT FT /product= type I TNF receptor
FT FT 256..318
FT FT /*tag= b
FT FT mat_peptide 319..1620
FT FT /*tag= c
FT FT misc_RNA 319..864
FT FT /*tag= d
FT FT /label= soluble_domain
FT FT /note= "may be 2 codons shorter or a few codons longer"
FT FT misc_feature 376..414
FT FT /*tag= e
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FT FT /note= "TBP-I derived sequence"
FT FT 850..858
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FT FT 889..957
FT FT /*tag= h
FT FT /label= transmembrane_domain
FT FT 385..504
FT FT /*tag= i
FT FT /number= 1
FT FT repeat_unit 505..633
FT FT /*tag= j
FT FT /number= 2
FT FT repeat_unit 634..756
FT FT /*tag= k
FT FT /number= 3
FT FT repeat_unit 757..858
FT FT /*tag= l
FT FT /number= 4
FT FT polyA_signal 2145..2150
FT FT /*tag= m
FT FT EP433900-A.
FT FT PN
FT FT 26-JUN-1991.
FT FT PD
FT FT 13-DEC-1990; 90BP-0124133.
FT FT PF
FT FT 12-JUL-1990; 90IL-0095064.
FT FT PR 13-DEC-1989; 89IL-0092697.
FT FT XX
FT FT (YEDA ) YEDA RES & DEV CO LTD.
FT FT PA
FT FT PI Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
FT FT PI Aderka D;
FT FT PI WPI: 1991-186774/26.
FT FT DR P-PSDB; AAR12550.
FT FT XX
FT FT XX Recombinant tumour necrosis factor binding protein I - prepd. by
FT FT PT transfecting eukaryotic cells with vector contg. deoxyribonucleic
FT FT PT acid encoding human type I TNF receptor or soluble domain
FT FT XX
FT FT PS Disclosure: Fig 1(D): 30pp; English.
FT FT XX
FT FT CC The Tumour Necrosis Factor Binding Protein I is the soluble form of
FT FT CC type I TNF-receptor and constitutes a fragment of the cell surface
FT FT CC form of this receptor, corresp. to its extracellular domain.
FT FT CC There is no characteristic poly(A) addition signal near the 3' end
FT FT CC of the cDNA. The sequence ACTAAG (tag m) may serve as an
FT FT CC alternative to this signal, but with low efficiency.
FT FT CC See also AAQ12212-15.
FT FT CC
FT FT Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other:

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:16:35 : Search time 2817 Seconds

(without alignments)
14132.992 Million cell updates/sec

Title: US-09-899-429a-1

Perfect score: 1368

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Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

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8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_ln:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_ln:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

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37: em_htg_vrt:*

38: em_sy:*

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40: em_htgo_mus:*

41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1368	100.0	1368	6	A29098	A29098 Synthetic D
2	1368	100.0	2112	9	HUMTNFR	M63121 Human tumor
3	1368	100.0	2194	9	BC010140	BC010140 Homo sapi
4	1366.4	99.9	2087	9	HUMTNFR	A33294 Human tumor
5	1366.4	99.9	2111	6	A26412	A26412 CDNA for (5
6	1366.4	99.9	2111	6	AX409713	AX409713 Sequence
7	1366.4	99.9	2111	9	HUMTNFR	M58286 Homo sapien
8	1366.4	99.9	2161	6	AR063330	AR063330 Sequence
9	1366.4	99.9	2161	9	HSTNFR1A	X55313 H. sapiens t
10	1366.4	99.9	2175	6	A43873	A43873 Sequence 1
11	1366.4	99.9	2175	6	A78738	A78738 Sequence 7
12	1366.4	99.9	2175	6	AR041076	AR041076 Sequence
13	1366.4	99.9	2175	6	I64751	I64751 Sequence 1
14	1366.4	99.9	2176	6	A19907	A19907 Synthetic n
15	1363.2	99.6	2062	6	A21522	A21522 TNF alpha 9
16	1360	99.4	2062	6	I43805	I43805 Sequence 24
17	1351.2	98.8	2061	6	A20255	A20255 55kd recept
18	1344.4	98.3	2109	9	AK056611	AK056611 Homo sapi
19	1323.2	96.7	2050	9	HUMTNFR	M60275 Human tumor
20	1106	80.8	1331	6	A29103	A29103 H. sapiens m
21	890.6	65.1	2171	4	AB051103	AB051103 Fells cat
22	861	62.9	2004	4	SSU19994	U19994 Sus scrofa
23	743.4	54.3	2115	10	AF329976	AF329976 Rattus no
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25	743.4	54.3	2130	6	AX401925	AX401925 Sequence
26	743.4	54.3	2130	10	RAT2NER	M63122 Rat tumor n
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30	741.8	54.2	2115	10	AF329981	AF329981 Rattus no
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32	690.4	50.5	2048	10	MUSTNFR1	M60468 Mouse tumor
33	690.4	50.5	2063	10	MMP5R	X59238 Murine mRNA
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37	685.4	50.1	2440	4	BTU0937	U90937 Bos taurus
38	632.8	46.3	6896	6	AR031375	AR031375 Sequence
39	632.8	46.3	6896	6	BD009743	BD009743 Compositi
40	632.4	46.2	6889	6	I26928	I26928 Sequence 2
41	596.8	43.6	600	6	A20257	A20257 Synthetic n
42	593.6	43.4	600	6	I43808	I43808 Sequence 47
43	514	37.6	1301	6	ARI31310	ARI31310 Sequence
44	514	37.6	1301	6	ARI34762	ARI34762 Sequence
45	510	37.3	510	6	A21525	A21525 Oligonucleo

ALIGNMENTS

RESULT 1

A29098 LOCUS 1368 bp DNA linear PAT 03-JUL-1995

DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.

ACCESSION A29098

VERSION A29098.1 GI:1248892

KEYWORDS

ORGANISM

SOURCE

synthetic construct.

synthetic construct.

artificial sequences.

REFERENCE

1 (bases 1 to 1368)

AUTHORS Hauptmann,R., Himmeler,A., Maurer-Fogy,I. and Stratowa,C.

TITLE TNF-receptor, TNF-binding protein and DNA coding therefor

JOURNAL Patent: EP 0393438-A 48 24-OCT-1990;

BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

Pred. No. is the number of results predicted by chance to have a

FEATURES	Location/Qualifiers
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	/db_xref="taxon:32630"
BASE COUNT	293 a 424 c 375 g 276 t
ORIGIN	

Query Match	100.0%;	Score 1368;	DB 6;	Length 1368;
Best Local Similarity	100.0%;	Pred. No. 1e-265;		
Matches 1368; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Db	1	ATGGCCCTCTCACCCTGACCTGCTCTGTGGCACTGGTGCTCCCTGAGACGTGTGGTG	60
QY	61	GGAATATATACCCCTTAGGGGTTATTGGACTGTCCTCTACCTAGGGGACAGGAGAAAGAGA	120
Db	61	GGAATATATACCCCTTAGGGGTTATTGGACTGTCCTCTACCTAGGGGACAGGAGAAAGAGA	120
QY	121	GATAGTGTGTGTCCCAAGGAAATATATACACCTCCAAATAATTCGATTTCTGTACC	180
Db	121	GATAGTGTGTGTCCCAAGGAAATATATACACCTCCAAATAATTCGATTTCTGTACC	180
QY	181	AAGGCCCAAAAGAACCTCTTGTACAATGACGTCCAGGCCCGGGGGCAGGATPAGGAC	240
Db	181	AAGGCCCAAAAGAACCTCTTGTACAATGACGTCCAGGCCCGGGGGCAGGATPAGGAC	240
QY	241	TGCAGGAGATGTGAGACGGGCTCCTTACCGCTTCAGAAAACCACTCAAGACACTGCTTC	300
Db	241	TGCAGGAGATGTGAGACGGGCTCCTTACCGCTTCAGAAAACCACTCAAGACACTGCTTC	300

Db	901	CCCGGTGACTGTGCCAACATCTTTGGGGCTCCCGCGAGAGAGTGGCAACACCTATCAGGGG	960
QY	961	GCTGACCCCATCTTTGGCGACAGCCCTGCGCTTCGACCCCATCCCAACCCCTTCAGAG	1020
Db	961	GCTGACCCCATCTTTGGCGACAGCCCTGCGCTTCGACCCCATCCCAACCCCTTCAGAG	1020
QY	1021	TGGGAGACAGCGCCGACACAGCCACAGACCTAGACACTGATGATACCCGCGAGCGCTGTAC	1080
Db	1021	TGGGAGAGACAGCGCCACACAGCCACAGAGCCTAGACACTGATGATACCCGCGAGCGCTGTAC	1080
QY	1081	GCCGTGTGTGAGAACGTGCCCCCGTTGGCGCTGGAAGAAATTGTGTGCGGCGCTTAGGGCTG	1140
Db	1081	GCCGTGTGTGAGAAAGTGCCTCCCGTTGGCGCTGGAAGAAATTGTGTGCGGCGCTTAGGGCTG	1140
QY	1141	AGCGACACAGAGATGATCGGCTGGAAGCTGCAGAAACGGGCGCTGCTGCGCGAGGGCGAA	1200
Db	1141	AGCGACACAGAGATGATCGGCTGGAAGCTGCAGAAACGGGCGCTGCTGCGCGAGGGCGAA	1200
QY	1201	TACACACATGCTGGGCACTGTGGAGGGGGGCGACGGCGCGCGGGGAGGGCCACGGCTGGAGCG	1260
Db	1201	TACACACATGCTGGGCACTGTGGAGGGGGGCGACGGCGCGCGGGGAGGGCCACGGCTGGAGCG	1260
QY	1261	CTGGGACGCGTGCCTCGGGACATGTGACCGTGTGGGTGTGCTGAGAGACATCGAGGAGGGG	1320
Db	1261	CTGGGACGCGTGCCTCGGGACATGTGACCGTGTGGGTGTGCTGAGAGACATCGAGGAGGGG	1320
QY	1321	CTTTTCGGGCGCGCGCGCGCTCCCGCGCGGCGCCAGTCTCTCAGANTGA 1368	
Db	1321	CTTTTCGGGCGCGCGCGCGCTCCCGCGCGGCGCCAGTCTCTCAGANTGA 1368	

QY	301	AGCTGCTCAAAATCCCAAAAGAAATGGGTCAGGTGAGATATCTTTTCCACAGTGGAC	360
Db	301	AGCTGCTCAAAATCCCAAAAGAAATGGGTCAGGTGAGATATCTTTTCCACAGTGGAC	360
QY	361	CGGACACACCGTGTGCTGCCTGCAGAGAACCGATGCCGCAATTAATGAGTGAACAACTT	420
Db	361	CGGACACACCGTGTGCTGCAGAGAAACCGATGCCGCAATTAATGAGTGAACAACTT	420
QY	421	TTCCAGAGCTTCAAATTTGCAGCTGTGCTCAATGGAGACCGTGGACCTTCCTCCAGAG	480
Db	421	TTCCAGAGCTTCAAATTTGCAGCTGTGCTCAATGGAGACCGTGGACCTTCCTCCAGAG	480
QY	481	AAACAGAACACCGTGTGCACCTGCATGACAGGTTCTTCTTAAGAGAAAAAGAGTGTTC	540
Db	481	AAACAGAACACCGTGTGCACCTGCATGACAGGTTCTTCTTAAGAGAAAAAGAGTGTTC	540
QY	541	TTCCGTGTACTAGTAAAGAAAGCTGAGATGGACAGAAATTTGGCTTACCCCAATTTGAG	600
Db	541	TTCCGTGTACTAGTAAAGAAAGCTGAGATGGACAGAAATTTGGCTTACCCCAATTTGAG	600
QY	601	AATGTTAAGGGCACGTGAGGACTCAGGCACACAGTGTGTTGGCCCTGATCATTTTCTTT	660
Db	601	AATGTTAAGGGCACGTGAGGACTCAGGCACACAGTGTGTTGGCCCTGATCATTTTCTTT	660
QY	661	GGCTTTGGCCTTTTATCCCTCCCTCTTATTTGGTTTAAATGATGGCTACCAAGGTGGAG	720
Db	661	GGCTTTGGCCTTTTATCCCTCCCTCTTATTTGGTTTAAATGATGGCTACCAAGGTGGAG	720
QY	721	TCCAAAGCTACTCCATTTGTTTGGGAAATGCACACCTAAAAAAGAGGGGAGCTTGAAT	780
Db	721	TCCAAAGCTACTCCATTTGTTTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTGAAT	780
QY	781	GGAATCTACTAAGAGCCCTGAGCCCAACCCAAAGCTTCAAGTCCCATCCAGGCTTAC	840
Db	781	GGAATCTACTAAGAGCCCTGAGCCCAACCCAAAGCTTCAAGTCCCATCCAGGCTTAC	840
QY	841	CCCAACCTGGGGCTCAATCCCGTGGCCAGTTCCACCTTCACCTCCAGCTCACTTAAC	900
Db	841	CCCAACCTGGGGCTCAATCCCGTGGCCAGTTCCACCTTCACCTTCAGCTCCACCTTAAC	900
QY	901	CCCGGTACTGTCCCAACTTTGGGGCTCCCGCAGAGAGGTGCACACCTTAACAGGG	960
Db	901	CCCGGTACTGTCCCAACTTTGGGGCTCCCGCAGAGAGGTGCACACCTTAACAGGG	960

RESULT 2					
HUMTNFRC LOCUS	DEFINITION	ACCESSION VERSION	SOURCE	ORGANISM	REFERENCE AUTHORS
	Human tumor necrosis factor receptor (TNF receptor) mRNA, complete cds.	M63121 M75861 M63121.1 GI:339755	tumor necrosis factor receptor. human cdna to mRNA.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
		1 (bases 1 to 2112)			Himmeler,A., Maurer-Fogy,I., Kronke,M., Scheurlich,P., Pfizematter,K., Lantze,M., Olsson,I., Hauptmann,R., Stratowa,C. and Adolf,G.R.
TITLE	Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein				
JOURNAL MEDLINE PUBMED	DNA Cell Biol.	9 (10), 705-715 (1990)			
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BASE COUNT      435 a      589 g      456 t
ORIGIN

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Best Local Similarity	100.0%	Pred. NC. 1e-265		
Matches 1368	0	Mismatches	0	Indels 0
				Gaps 0

QY	1	ATGGGGCCCTCTCCACCGCGCCGAGACCTGGCTGCTCCAGCTGGTTGGTG	60
Dp	207	ATGGGGCCCTCTCCACCGCGCTGACCTGGCTGCTCCACTGGTCTCCTGGAGCTGTTGGTG	266
OY	61	GGAAATATACCCCTCAGGGGGTTATTGGACATGGTCCCTCACCCTAGGGGACAGGAAGA	120
Dp	267	GGAAATATACCCCTCAGGGGGTTATTGGACATGGTCCCTCACCCTAGGGGACAGGAAGA	326
OY	121	GATAGTGTGTGTCCCCAGGAGAAATATATCCACCCTCAAAATAATATTCATTGTGCTGAC	180
Dp	327	GATAGTGTGTGTCCCCAGGAGAAATATATCCACCCTCAAAATAATATTCATTGTGCTGAC	386
OY	181	AAGTGCACAAAGAACCTACTTGTACAAATGACTGTCCAGGCCGGGGGACGATATCGGAC	240
Dp	387	AAGTGCACAAAGAACCTACTTGTACAAATGACTGTCCAGGCCGGGGGACGATATCGGAC	446
OY	241	TTCAGGGGAGTGTGAGACGGGCTCCTTCACCGGCTTCAGAAACACACTCAGACACGCTC	300
Dp	447	TTCAGGGGAGTGTGAGACGGGCTCCTTCACCGGCTTCAGAAACACACTCAGACACGCTC	506
OY	301	AGCTGCTCCAAATGCCCCAGAAAGAAATGGGTCAAGSTGAGAAATCTCTTCTTGACAGTGGAC	360
Dp	507	AGCTGCTCCAAATGCCGAAGGAATGGGTCAAGSTGAGAAATCTCTTCTTGACAGTGGAC	566
OY	361	CGGACACCGTGTGTGGCTTCAGAGAAAGAACCACTACCGGCATTATTTGGAGTGAACCTT	420
Dp	567	CGGACACCGTGTGTGGCTTCAGAGAAAGAACCACTACCGGCATTATTTGGAGTGAACCTT	626
OY	421	TTTCAGAGCTTCAATTTCACACCTCTGACCTCAATGGAGACCGTGCACCTTCGCGCCAGAG	480
Dp	627	TTTCAGAGCTTCAATTTCACACCTCTGACCTCAATGGAGACCGTGCACCTTCGCGCCAGAG	686
OY	481	AAACAGAACACCGTGTGTCACCTGCATGCAAGTTTCTTCTAAGAGAAAAAGAGTGTCTC	540
Dp	687	AAACAGAACACCGTGTGTCACCTGCATGCAAGTTTCTTCTAAGAGAAAAAGAGTGTCTC	746
OY	541	TTCCTGTAGTAACTGTAAAGAAAAGCCTGGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG	600
Dp	747	TTCCTGTAGTAACTGTAAAGAAAAGCCTGGAGTGCAGCAAGTTGTGCTTACCCAGATTGAG	806
OY	601	AATGTTAAAGGACACTGAGCACTCAGGCACACAGTCTGTTGCCCTGGTCAATTTCTTT	660
Dp	807	AATGTTAAAGGACACTGAGCACTCAGGCACACAGTCTGTTGCCCTGGTCAATTTCTTT	866
OY	661	GGTCTTGGCTTTTATCCCTCTCTTCAATTTGGTTAATGTATCGGTACCAAGGTGAGAG	720
Dp	867	GGTCTTGGCTTTTATCCCTCTCTCTTCAATTTGGTTAATGTATCGGTACCAAGGTGAGAG	926
OY	721	TTCCAAGCTTACTTCATTTGTTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTAA	780
Dp	927	TTCCAAGCTTACTTCATTTGTTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTAA	986
OY	781	GGAACTACTACTAAGCCCTGGGCCCAAAACCMAAGTTTAGTCCCACTCAGGCTTACAC	840
Dp	987	GGAACTACTACTAAGCCCTGGGCCCAAAACCMAAGTTTAGTCCCACTCAGGCTTACAC	1046
OY	841	CCCAACCTGGGCTTCAGTCCCGTGGCCCAAGTTCCACCTTCACCTCAGCTCCACTATAC	900
Dp	1047	CCCAACCTGGGCTTCAGTCCCGTGGCCCAAGTTCCACCTTCACCTCAGCTCCACTATAC	1106

QY	901	CCGGGTGACGTGCCCAACATTGGGGCTCCCGGCAGAGAGGTGGCACACCCATTACAGGG	960
Db	1107	CCGGGTGACGTGCCCAACATTGGGGCTCCCGGCAGAGAGGTGGCACACCCATTACAGGG	1166
QY	961	GCTGACCCCATCTTTGGGACACACCTCTGCCTTCAGACCCCATCCCAACCCCTTTCAGAG	1020
Db	1167	GCTGACCCCATCTTTGGGACACACCTCTGCCTTCAGACCCCATCCCAACCCCTTTCAGAG	1226
QY	1021	TGGGAGGACAGCGGCCCCACACAGCCACACAGACCTAGACACTGATGACCCCGGACGCTGTAC	1080
Db	1227	TGGGAGGACAGCGGCCCCACACAGCCACACAGACCTAGACACTGATGACCCCGGACGCTGTAC	1286
QY	1081	GCCGTGTGGAGAAAGTGCCTCCCTCTTGGGCTTGGAGAAATTGTTGTCGGCGCTAGGGCTG	1140
Db	1287	GCCGTGTGGAGAAAGTGCCTCCCTCTTGGGCTTGGAGAAATTGTTGTCGGCGCTAGGGCTG	1346
QY	1141	AGCGACCAAGAGATCGATGGCTGGAGCTGCAGAAACGGGGCTGCCTCGCGAGGCGCAA	1200
Db	1347	AGCGACCAAGAGATCGATGGCTGGAGCTGCAGAAACGGGGCTGCCTCGCGAGGCGCAA	1406
QY	1201	TACACATGCTGGGACGCTGGAGGGGGGCGACAGCGCGGGGAGGCGGACGCTGGAGGTG	1260
Db	1407	TACACATGCTGGGACGCTGGAGGGGGGCGACAGCGCGGGGAGGCGGACGCTGGAGGTG	1466
QY	1261	CTGGGACGCGTGTCTCCGAGACATGAGACCTGTCTGGGCTCTTGGAGAGACATCGAGGAGCG	1320
Db	1467	CTGGGACGCGTGTCTCCGAGACATGAGACCTGTCTGGGCTCTTGGAGAGACATCGAGGAGCG	1526
QY	1321	CTTTGCGGGCCCCGGCGCCCTCCCGCGCGCGGCCCAATTCTTTCAGATTGA	1368
Db	1527	CTTTGCGGGCCCCGGCGCCCTCCCGCGCGCGGCCCAATTCTTTCAGATTGA	1574

RESULT 3					
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LOCUS	BC010140	2194 bp	mRNA	linear	PRI 12-JUL-2001
DEFINITION	Homo sapiens, tumor necrosis factor receptor superfamily, member 1A, clone MGC:19588, IMAGE:4131360, mRNA, complete cds.				
ACCESSION	BC010140				
VERSION	BC010140.1	GI:14603367			
KEYWORDS	MGC.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2194)				
AUTHORS	Straussberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov				
COMMENT	Contact: MGC help desk				

CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: [http://www.nisc.nih.gov/
 nisc.mcgenhtml.nih.gov](http://www.nisc.nih.gov/nisc.mcgenhtml.nih.gov)
 Contact:
 Shevchenko, Y., Wetherby, R.W., Beekström-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Mastello, C., Mastilan, S.D., McLoesley, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantipop, S., Thomas, P.J.,
 Tlionson, E.E., Touchman, J.W., Tsaurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

MEDLINE 90235285
PUBMED 2158863
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by T.Schall, 26-MAR-1990.
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Best Local Similarity 99.9% Pred. No. 2.1e-265;
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ACCESSION A26412
VERSION A26412.1 GI:904968
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SOURCE
ORGANISM
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AUTHORS Brockhaus, M., Dembic, Z., Genz, R., Lesslauer, W., Loetscher, H. and
Schlaeger, E.J.
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Query Match	99.9%;	Score 1366.4;	DB 6;	Length 211;
Best Local Similarity	99.9%;	Pred. No. 2.1e-265;		
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OY	61	GGAAATATACCCCTCAGGGGTTATTGGAGCTGGTCCCTACCTAGGGGACAGGAGAGAGA	120
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OY	181	AAGGCGCAAGGAAGACCTACTGTTACAAATGACGTGCAGGCGCGGGGACGAGTACGGAC	240
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Db	487	AGCTGCTCAAAATCCGGAAGGAATGGGTGAGATCTCTTTGTCACAGTGGAC	546
OY	361	CGGGACACCGGTGTGGCTGCGAGGAACAACCACTGACCGCATTTATTTGAGTGAACCTT	420
Db	547	CGGGACACCGGTGTGGCTGCGAGGAACAACCACTGACCGCATTTATTTGAGTGAACCTT	606
OY	421	TTCCAGTGCCTCAATTTGAGCGCTGGCTCAATGGGACGCTGCAACCTCTGTCGACGAG	480
Db	607	TTCCAGTGCCTCAATTTGAGCGCTGGCTCAATGGGACGCTGCAACCTCTCTCCAGGAG	666
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Db	667	AAACGAACACCGGTGACACTGCGCAATGACAGTTCCTTTAGAGAAAACGAGTGTGC	726
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Db	787	AATGTTAAGGGCACTGAGGACATCAGGACACCAAGTGTGTCGCCCTCGGTCAATTTCTTT	846
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Db	847	GCTGTTTCCCTTTATATCCCTCTCTTCAATTTGTTTATGTATGCTATCCAAACGTTGAG	906
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Db	967	GGAACTACTAATAAGCCCTGGGCCCAAAACCCAAAGCTTAGTCCCACTGCAGGCTTACAC	1026
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Db	1027	CCCAACCTGGGCTTCACTCCCGTGGCCAGTTCCACCTTCACTCCAGCTCCACCTATAC	1086
OY	901	CCCGGTACACTGTCCCAACTTTGGGGCTCCCGGAGAGAGTGTGGCAACCCATATAGGGG	960
Db	1087	CCCGGTACACTGTCCCAACTTTGGGGCTCCCGGAGAGAGTGTGGCAACCCATATAGGGG	1146
OY	961	GCTAACCCTATCTTTGGGAGACAGCCCTTGCCCTCGACCCCATCCCAACCCCTTTCAGAG	1020
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Db	1267	GCCGTGGTGAGAAAGTGCCCCCGTTGGCTGTGAGAGGAATTTGTCGGGCGCTTAGGGCTG	1366
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Db	1327	AGGCACCAAGAGATCGATGTGGCTGGAGAGTCGAAAGAGGCGTGGCTGGGCGAGGCGCA	1386
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LOCUS	2111 bp	DNA	Linear
DEFINITION	AX409713 Sequence 2360 from Patent WO0229103.		
			PAT 14-JUN-2002

KEYWORDS
SOURCE
human.

ORGANISM	Homosapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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REFERENCE	1
AUTHORS	Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J. G.
TITLE	Gene expression profiles in liver cancer
JOURNAL	Patent: WO 0229103-A-2360 11-APR-2002;

FEATURES	GENE.LOGIC INC (US)
source	location/Qualifiers
	1. .2111

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Dh 1507 CTTTGG 1554
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LOCUS Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
DEFINITION M58286 M33480
ACCESSION M58286.1 GI:339753
VERSION
KEYWORDS tumor necrosis factor receptor.
SOURCE Human cell line HL60, CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M., Tabuchi, H., and Lesslauer, W.
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor
JOURNAL Cell 61 (2), 351-359 (1990)
MEDLINE 90235284
PUBMED 2158862
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Query Match 99.9%; Score 1366.4; DB 9; Length 2111;
Best Local Similarity 99.9%; Pred. No. 2,1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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D	b	307	GATATGTGTGTCCCAAGAAAAATATATACACCTTCACAAATATTCGATTGTGTGTACC	366
O	y	181	AAGTCCCAAAAGAACTACTTGTACAAATGACTGTCCAGGGCCGGGGGACAGATACAGAC	240
D	b	367	AAGTCCCAAAAGAACTACTTGTACAAATGACTGTCCAGGGCCGGGGGACAGATACAGAC	426
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D	b	487	AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTTTTTCACAGTGGAC	546
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D	b	547	CGGGACACCGGTGTGGGTGTGAGAGAAACCACTACCGGATATTGAGGTAAAACTT	606
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D	b	607	TTCCAGTCTTCAATTGAGAGCTGTGCTCAATAGGGACCGGTGACCTTCCTGCCAGAG	666
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D	b	787	AATGTTAAGGCACTGAGAGCACTGAGGACACAGTGTGTGGCCCTGGTCAATTTCTTT	846
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D	b	907	TCCAAGCTTACTCATTTGTTTGTGGGAAATGCACACCTGAAAAAGAGGGGAGCTTGA	966
O	y	781	GGAACTACTATTAGCCCGTGGCCCCCAACCCAGAGCTCAGTCCCACTCAGCTCATATACC	840
D	b	967	GGAACTACTATTAGCCCGTGGCCCCCAACCCAGAGCTCAGTCCCACTCAGCTCATATACC	1026
O	y	841	CCCAACCTTGGGCTTCAGTCCCGTGGCCCCAGTTCACACTTCACCTCAGCTCAGCTCATATACC	900
D	b	1027	CCCAACCTTGGGCTTCAGTCCCGTGGCCCCAGTTCACACTTCACCTCAGCTCAGCTCATATACC	1086
O	y	901	CCCGGTGACTCTCCCAACTTTTGGGGCTCCCGCAGAGAGGTGGACACCTCATATCAGAGG	960
D	b	1087	CCCGGTGACTCTCCCAACTTTTGGGGCTCCCGCAGAGAGGTGGACACCTCATATCAGAGG	1144
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D	b	1147	GCTGACCCCAATCTTTGGGAGACGGCTCGCTCCGAGCCCATCCCAACCCCTTTCAGAG	1206
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D	b	1207	TGGGAGCAGACGGCCCAACAGCAACAGAGCTTGAACACTGATGACCCCGCAGCGCTTAC	1266
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Dd	1447	CAGGACGCGTCTCCGCGACATGGAACCTGTCGGGCTGCTTGAGACATGAGAGCGG	1506
Oy	1321	CTTTGGCGGCCCCGCGCCCTCCCGCCGCGCCAGCTCTTCAGATTGA	1368
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified. 1 (bases 1 to 2161)		
AUTHORS	Baker, B.F. and Cowser/L.M.		
TITLE	Antisense inhibition of TNFRI expression		
JOURNAL	Patent: US 6007995-A 1 28-DEC-1999;		
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RESULT 9
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DEFINITION H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
ACCESSION X53513
VERSION X53513.1 GI:37223
KEYWORDS TNF-R gene; tumor necrosis factor receptor 1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Nohar,Y., Kemper,O., Brakebusch,C., Englemann,H., Zhang,R.,
Aderka,D., Holtmann,H. and Wallach,D.

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TITLE Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
for the type I TNF-R, cloned using amino acid sequence data of its
soluble form, encodes both the cell surface and a soluble form of
the receptor.
JOURNAL EMBO J. 9 (10), 3269-3278 (1990)
MEDLINE 91006021
PUBMED 1698610
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BASE COUNT 459 a 642 c 604 g 456 t
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Query Match 99.9%; Score 1366.4; DB 9; Length 2161;
Best Local Similarity 99.9%; Pred. No. 2,1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ATGGGCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
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Oy 61 GGAATATACCCCTCAGGGGTTATGAGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 316 GGAATATACCCCTCAGGGGTTATGAGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Oy 121 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC 180
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RESULT 10
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DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS unidentifed.

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ORGANISM unidentifed
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R
        derived peptides and antibodies against the proteases inhibiting
        the shedding
JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;
COMMENT YEDA RES & DEV (IL)
        Other publication ZA 9407962 951121
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Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No.2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0;
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Db 256 ATGGGCTCTCTCCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
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Dd	976	TCCAAGCTCTACTCCATTGTGTGTGGAAATTCGACACTGTAAAAAGAGGGGAGCTTAA	1035
OY	781	GGAATCTACTTAAACCCCTGGCCCCCAAACCAGCTTCAGTCCCATTCAGAGCTTCAC	840
Dd	1036	GGAATCTACTTAAACCCCTGGCCCCCAAACCAGCTTCAGTCCCATTCAGAGCTTCAC	1095
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Dd	1096	CCCACCTTGCGCTCAGTCCCGTGCCTCAGTTCACCTTCACCTCCAGCTTCACCTATAC	1155
OY	901	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGGACAGAGTGTGGACCAACCTATACGGG	960
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OY	1261	CTGGGACGCGTGTCTCCGCGACATGAGACCTGTGTGGGCTCCTCTGGAGACATCGAGAGGCG	1320
Dd	1516	CTGGGACGCGTGTCTCCGCGACATGAGACCTGTGTGGGCTCCTCTGGAGACATCGAGAGGCG	1575
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DEFINITION	Sequence 7 from Patent EP0568925.	DNA	linear
ACCESSION	A78738		PAT 19-OCT-1999
VERSION	A78738.1	GI:6090341	
KEYWORDS	unidentified. unclassified.		
SOURCE	ORGANISM		
REFERENCE	1 (bases 1 to 2175)		
AUTHORS	Brakebusch,C. and Wallach,D.		
TITLE	TNF RECEPTOR ACTION MODULATION		
JOURNAL	Patent: EP 0568925-A 7 10-NOV-1993; YEDA RES & DEV (IL)		

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Best Local Similarity	99.9%; Pred. No. 2,1e-265;
Matches 1367; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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OY	421 TTCCAGTCTTCAMPTGACAGCTCTGGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 480
Db	676 TTCCAGTCTTCAMPTGACAGCTCTGGCTCAATGGGACCGTGCACCTCTCTGCCAGAG 735
OY	481 AAACAGAACACACGTTGCACCTGECATGACAGGTTTTCTTTCTAAGAGAAAAACGAGTGTGC 540
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OY	541 TCCTGTAGTAACTGTAAGAAAAAGCCTTGAAGTGCACGAAGTTGTGCTTACCCAGATTGAG 600
Db	796 TCCTGTAGTAACTGTAAGAAAAAGCCTTGAAGTGCACGAAGTTGTGCTTACCCAGATTGAG 855
OY	601 AATGTTAAGGGGACATGAGAGACTCAGGGACACAGTGTGTGGCCCTGGCATTTTCTTT 660
Db	856 AATGTTAAGGGGACATGAGAGACTCAGGGACACAGTGTGTGGCCCTGGCATTTTCTTT 915
OY	661 GGCTCTTCCCTTTATCCCTCTCTTCATTTGGTTTAATGTATGCTTACCAAGGGTGAAG 720
Db	916 GGCTCTTCCCTTTATCCCTCTCTTCATTTGGTTTAATGTATGCTTACCAAGGGTGAAG 975
OY	721 TTCGAAGCTCTACTCATTTGTTTGGGAAATCGACACTTAATAAAGAGGGGAGCTTGAA 780
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OY	781 GGAATCTACTTAAGCCCGTGGCCCAAACCCAAAGCTTCAGTCCCACTCAGAGCTTCACC 840
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 Best Local Similarity 99.9%; Pred. No. 2.1e-265;
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DB 316 GGAATATACCCCTCAGGGGTTATGAGACTGGTCCCTCAGCTAGGGGAGAGAGAGA 375
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ACCESSION A21522
VERSION A21522.1 GI:579599
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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BASE COUNT 429 a 617 c 573 g 443 t
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Best Local Similarity 99.8%; Pred. No. 9.3e-265;
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Oy 421 TTCCAGTCTTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGAG 480
Db 575 TTCCAGTCTTCAATTTGACAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGAG 634
Oy 481 AAACAGAACACCGTGTGCACCTGTCATGAGTTCCTTTCTAAGAAAAACGAGTGTGC 540
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Oy 541 TCCTGTAGTAATGTAAAGAAAGCCTGAGTGTGCAGAGTGTGCTACCCAGATTGAG 600
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Db 755 AATGTTAAGGAGCAGAGAGTGTGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 814
Oy 661 GGTCTTGGCTTTTATCCCTCTCTTCAATGGTTCATGATGCTTACCAACGATGGAAG 720
Db 815 GGTCTTGGCTTTTATCCCTCTCTTCAATGGTTCATGATGCTTACCAACGATGGAAG 874
Oy 721 TCCAGCTCTACTCCATTTGTTGTGGAAATGACACCTGAAAGAGGGGAGCTTGA 780
Db 875 TCCAGCTCTACTCCATTTGTTGTGGAAATGACACCTGAAAGAGGGGAGCTTGA 934
Oy 781 GGAACCTACTACTAAGCCCTGCGCCCAAAACCAAGCTTCAGTCCACTCCAGCTTCAC 840
Db 935 GGAACCTACTACTAAGCCCTGCGCCCAAAACCAAGCTTCAGTCCACTCCAGCTTCAC 994
Oy 841 CCCACCTGTGGGCTTCAAGTCCGCTGCGCAGTTCACCTTCACCTCCAGCTTCACCTATAC 900
Db 995 CCCACCTGTGGGCTTCAAGTCCGCTGCGCAGTTCACCTTCACCTTCACCTATAC 1054
Oy 901 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGTGCACACCTATCAGGG 960
Db 1055 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGTGCACACCTATCAGGG 1114
Oy 961 GCTGACCCCATCTTGGCGAGAGCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
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Oy 1021 TGGGAGAGACGCGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGCAGCCTGTAC 1080
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Oy 1261 CTGGGAGCGGTGTCTCCGCGACATGAGACCTGCTGGGCTGTGAGAGACATCGAGAGCG 1320
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Search completed: December 4, 2002, 21:07:51
Job time : 2847 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2002, 19:18:10 ; Search time 2059 Seconds
(Without alignments)
10760.285 Million cell updates/sec

Title: US-09-899-429A-1
Perfect score: 1368
Sequence: 1 atggagcttcctccacgtgcc.....cgcacagcttcctcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estnu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	809.8	59.2	1076	14	BM923204 AGENCOURT
2	803.6	58.7	931	14	BQ723672 AGENCOURT
3	764.6	55.9	957	9	AL559050 AL559050
4	703.6	51.4	741	13	B1860918 B1860918
5	689	50.4	889	9	AU117362 AU117362
6	682.4	49.9	761	9	AU131978 AU131978

7	680	49.7	942	9	AL529836	AL529836
8	679.8	49.7	1070	13	BM546826	BM546826 AGENCOURT
9	678.2	49.6	975	9	AL577008	AL577008
10	669	48.9	669	14	BM742388	BM742388 K-EST0015
11	668.6	48.9	974	12	BG180101	BG180101 602329676
12	667.8	48.8	696	14	BM989994	BM989994 UI-H-D10-
13	667	48.8	718	12	BG680679	BG680679 602626965
14	647.2	47.3	994	14	BM800044	BM800044 AGENCOURT
15	638.4	46.7	837	9	AL522989	AL522989
16	630.4	46.1	769	9	AL522226	AL522226
17	628.6	46.0	916	13	B1757305	B1757305 603029519
18	625	45.7	636	12	BG035257	BG035257 602324771
19	620.4	45.4	1131	13	BM467058	BM467058 AGENCOURT
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21	605.2	44.2	969	12	BE871809	BE871809 601448388
22	602	44.0	602	14	BM791206	BM791206 K-EST0071
23	601.4	44.0	643	12	BG680356	BG680356 602629252
24	596.2	43.6	859	13	B1870917	B1870917 60394462
25	590.8	43.2	627	14	BM763879	BM763879 K-EST0045
26	588	43.0	811	12	BF342334	BF342334 602013123
27	585.4	42.8	872	13	B1769006	B1769006 603058164
28	576	42.1	576	14	BM820201	BM820201 K-EST0088
29	573.4	41.9	575	14	BM705174	BM705174 UI-E-C11-
30	564	41.2	845	13	AL125021	AL125021
31	559.4	40.9	739	13	B1520191	B1520191 603071439
32	559	40.9	859	9	AU124446	AU124446
33	559	40.9	936	12	BG681438	BG681438 602628106
34	557.2	40.7	872	14	BQ723589	BQ723589 AGENCOURT
35	556.6	40.7	767	9	AU142156	AU142156
36	549	40.1	549	14	BM708362	BM708362 UI-E-C11-
37	546	39.9	546	14	BM782977	BM782977 K-EST0060
38	542	39.6	1055	13	BM555065	BM555065 AGENCOURT
39	541.8	39.6	915	14	BQ881180	BQ881180 AGENCOURT
40	541.4	39.6	702	12	BF344496	BF344496 602014902
41	541	39.5	971	12	BE876920	BE876920 601488490
42	540.6	39.5	772	9	AU137990	AU137990
43	533.6	39.0	823	13	B1766980	B1766980 603054065
44	530.4	38.8	532	14	BM755879	BM755879 K-EST0033
45	529.4	38.7	1008	14	BQ719773	BQ719773 AGENCOURT

ALIGNMENTS

RESULT 1
BM923204
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM923204 1076 bp mRNA linear EST 12-MAR-2002
AGENCOURT.6625801 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758757
5' mRNA sequence.
BM923204
BM923204.1 GI:19373583
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 1076)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12803 row: b column: 06
High quality sequence stop: 727.
Location/Qualifiers
1. 1076

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5758757"
/lab.host="NIH_MGC_116"
/ab.host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPOrt6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb.
Insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

BASE COUNT      206 a      356 c      303 g      205 t      6 others
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Best Local Similarity 99.4%; Pred. No. 2.1e-189;
Matches 811; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 553 TGTAAAGAAAGCTGGAGATGACAGAGTGTGCTTACCCAGATTGAGATTGTAAGGCG 612
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Db 14 TGTAAAGAAAGCTGGAGATGACAGAGTGTGCTTACCCAGATTGAGATTGTAAGGCG 73

QY 613 ACTGAGAGACTCAGGACCAAGTGTGTTGCCCTGGTCATTTCTTTGGTCTTGGCCTT 672
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Db 74 ACTGAGAGACTCAGGACCAAGTGTGTTGCCCTGGTCATTTCTTTGGTCTTGGCCTT 133

QY 673 TTATCCCTCCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 732
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Db 134 TTATCCCTCCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 193

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Db 194 TCCATGTTGTGGGAATGACACTGAAAAAGAGGGAGCTTGAAGAACTACTACTACT 253

QY 793 AAGCCCTTGGCCCAAGACCTTCACTCCAGCTTCAAGGCTTCAACCCCACTGGGCG 852
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Db 254 AAGCCCTTGGCCCAAGACCTTCACTCCAGCTTCAAGGCTTCAACCCCACTGGGCG 313

QY 853 TTTCAGTCCCGTGCAGATTCACCTTACCTTCAGCTTCACTTATACCCCGGTGACTGT 912
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Db 314 TTTCAGTCCCGTGCAGATTCACCTTACCTTCAGCTTCACTTATACCCCGGTGACTGT 373

QY 913 CCCAATTGGGGCTCCCGCAGAGAGTGGGACCAACCTTATAGGGGGCTGACCCCATC 972
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QY 973 CTTCGACAGCCCTCCGCTCCGACCCATCCCAACCCCTTCAAGAGTGGAGAGCAG 1032
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Db 434 CTTCGACAGCCCTCCGCTCCGACCCATCCCAACCCCTTCAAGAGTGGAGAGCAG 493

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QY 1093 AAGGTGCCCCCTTGGCTGCGTGGAGAAATTCGTGCGGCGCTAGGGCTGAGCGACGAG 1152
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QY 1153 ATCGATCGGCTGGAGCTGAGAGAGGGGGCTGCTGCGGAGGCGGCAATACAGCATGCG 1212
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QY 1213 GCGACCTGGAGGCGGCGACGCGCGCGGCGAGGCGACGCTGAGTGTGGGAGCGCTG 1272
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QY 1273 CTCGCGGACATGAGACTGCTGGGCTGCTGAGAGACATGAGAGAGGCGCTTTGCGGCGCC 1332
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Db 734 CTCGCGGACATGAGACTGCTGGGCTGCTGAGAGACATGAGAGAGGCGCTTTGCGCCCG 793
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Db 794 GNGCGCTTCGCGCGCGGCGGCGAGCTTTCATGTA 829

RESULT 2
B0723672
LOCUS
DEFINITION
AGENCOURT_8489850 lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6184295 5', mRNA sequence.
B0723672
ACCESSION
B0723672
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 931)
NIH-MGC http://mgi.nhl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@dbi-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13573 row: d column: 24
High quality sequence stop: 607.
Location/Qualifiers
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/clone="IMAGE:6184295"
/lab.host="NIH_MGC_116"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/ab.host="DH10B"
/Note="Vector: PCMV-SPOrt6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCCG-3' and
5'-GACTAGTCTAGATCGGAGCGGCGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT      218 a      283 c      224 g      204 t      2 others
ORIGIN
Query Match      58.7%; Score 803.6; DB 14; Length 931;
Best Local Similarity 95.0%; Pred. No. 7e-188;
Matches 862; Conservative 0; Mismatches 40; Indels 5; Gaps 3;

QY 111 GGAGAAGAGATGATGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGAT 170
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Db 1 GGAGAAGAGATGATGTGTGTCGCCAAGAAATATATCCACCCCTCAAAATATTCGAT 60

QY 171 TTGCTTACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGGCGCGGGGCA 230
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Db 61 TTGCTTACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGGCGCGGGGCA 120

QY 231 GGATAGGAGTGCAGGAGATGTGAGAGCGGCTCTTACCGCTTCCAGAAACCACTCAG 290
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Db 121 GGATAGGAGTGCAGGAGATGTGAGAGCGGCTCTTACCGCTTCCAGAAACCACTCAG 180

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Oy	721	TCCAAAGCTTACTCATTGTTTGCGGAATGCACACCGAAAAA	765
Dd	913	TCCAAGCTTACTCCATTGTGTTGGGAAATGCACACCGAAAAA	957
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DEFINITION	603390284F1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:5399108 5' ,		
ACCESSION	B1860918		
VERSION	B1860918.1	GI:16001653	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 741)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov//		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs@email.nih.gov		
	Tissue Procurement: DCDN/DTP		
	cDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)		
	DNA sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LMNL at:		
	http://image.lnl.gov		
	Plate: LRAM12017 row: h column: 21		
	High quality sequence stop: 740.		
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	/note="Organ: breast; Vector: pCMV-Sport6; Site:1: NotI;		
	Site:2: SalI; Cloned unidirectionally; oligo-dt primed.		
	Average insert size 1.383 kb. Library enriched for		
	full-length clones and constructed by Life Technologies.		
	Note: This is a NIH_MGC Library."		
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ORIGIN			
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	Best Local Similarity	98.5%; Pred. No.3.5e-163;	
	Matches 731; Conservative	0; Mismatches 9; Indels 2; Gaps 2;	
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Oy	317	GAAGAAGATGGGTGAGATCTCTCTTGACAGAGTGGACCGGACACCGTGTG	376
Dd	61	GAAGAAGATGGGTGAGATCTCTCTTGACAGAGTGGACCGGACACCGTGTG	120
Oy	377	GCTGAGAGAAACACAGTACCGCATTTTGGAGTGAATACTTTCCAGTGTCAATT	436
Dd	121	GCTGAGAGAAACACAGTACCGCATTTTGGAGTGAATACTTTCCAGTGTCAATT	180
Oy	437	GCAGCTCTGGCTCAATGGAGACCGTGCCTCTGTCAGAGAAACAGAACCCGCTG	496
Dd	181	GCAGCTCTGGCTCAATGGAGACCGTGCCTCTGTCAGAGAAACAGAACCCGCTG	240
Oy	497	GCACCTGCATGCAAGTTCTTTCTTAAGAGAAAAGCATGTGTCTCTGTAGTAAGTGA	556
Dd	241	GCACCTGCATGCAAGTTCTTTCTTAAGAGAAAAGCATGTGTCTCTGTAGTAAGTGA	300
Oy	557	AGAAAAGCCTGGAGTGCAGAAATGTGTCCCTACCCACAGATTGAGANTCTTAAGGCACTG	616

Db	301	AGAAAAAGCTGGAGTGCACGAAAGTGTGTGCTACCCCAATTTGAGATGTAAAGGACACTG	360
QY	617	AGGACTCAGGACACACAGTGTGTGCTGTGCCCCGTGTCATTTTCTTTGGTCTTTGGCCCTTTAT	676
Db	361	AGGACTCAGGACACACAGTGTGTGCCCCGTGTCATTTTCTTTGGTCTTTGGCCCTTTAT	420
QY	677	CCCTCCTCTCTCATTTGGTTTAATGTATTCGTCTACCAACGGGTGGAAGTCCAAAGCTCTACTCCA	736
Db	421	CCCTCCTCTCTCATTTGGTTTAATGTATTCGTCTACCAACGGGTGGAAGTCCAAAGCTCTACTCCA	480
QY	737	TTGTTTGTGGGAATTCGACACCTGAGAAAAAGAGGGGAGCTTGAAGAATCTACTATAAGC	796
Db	481	TTGTTTGTGGGAATTCGACACCTGAGAAAAAGAGGGGAGCTTGAAGAATCTACTATAAGC	540
QY	797	CCCTGGCCCCAAACCCAAAGCTTCAGTCCACATCCAGGCTTACCCCCAACCTGTGGCTTTCA	856
Db	541	CCCTGGCCCCAAACCCAAAGCTTCAGTCCACATCCAGGCTTACCCCCAACCTGTGGCTTTCA	600
QY	857	GTCCCGGTGCGCCAGTTTCACACTTCACCTCAGTCCAGTCCACATATACCCCGGTGACTGTCCA	916
Db	601	GTCCCGGTGCGCCAGTTTCACACTTCACCTCAGTCCAGTCCACATATACCCCGGTGACTGTCCA	660
QY	917	ACTTTGGCGGCTCCCGCAGAGAGTGGGACACACCCCTATCA -GGGGGCTGACCCCATTCCTT	975
Db	661	ACTTTGGCGGCT -CCCGCAGAGAGTGGGACACACCCCTATCAAGGGGGGCTGACCCCATTCCTT	719
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Db	720	GGCAGACGCCCTCGCCTCGGACC 741	
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DEFINITION	AU117362	HEMBAL Homo sapiens	cdna clone HEMBAL001229 5', mRNA
ACCESSION	AU117362		
VERSION	AU117362.1	GI:10932324	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Iwatsugi, T.		
TITLE	HRI human cDNA project		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1. 889 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HEMBAL001229" /clone_1db="HEMBAL" /tissue_type="whole embryo, mainly head" /dev_stage="embryo, 10 weeks" /note="Vector: PME18SFL3"		
FEATURES	167 a	301 c	249 g
SOURCE	166 t	6	others
BASE COUNT			
ORIGIN			

Query Match 50.4%; Score 689; DB 9; Length 889;
 Best Local Similarity 99.4%; Pred. No. 1.5e-159;
 Matches 700; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 665 TTGTCCTTTATCCCTCTCTTCATTTGTTAATGATATGCTACCAACGGTGAAGTCCA 724
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 DB 1 TTTGGCTTTATCCCTCTCTTCATTTGTTAATGATATGCTACCAACGGTGAAGTCCA 60
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OY 725 AGCTTACTCATTGTTGTTGGAAATGACACCTGAAAGAGGGAGCTTGAAGAA 784
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 DB 61 AGCTTACTCATTGTTGTTGGAAATGACACCTGAAAGAGGGAGCTTGAAGAA 120
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OY 785 CTACTACTAAGCCCTGGCCCAACCAAGCTTCACTCCACTCCAGGCTTCAACCCCA 844
 |||||
 DB 121 CTACTACTAAGCCCTGGCCCAACCAAGCTTCACTCCACTCCAGGCTTCAACCCCA 180
 |||||

OY 845 CCTTGGGCTTCACTGCTCCGTCACCTTCACCTTCAGCTTCACCTTACCCCG 904
 |||||
 DB 181 CCTTGGGCTTCACTGCTCCGTCACCTTCACCTTCAGCTTCACCTTACCCCG 240
 |||||

OY 905 GTGACTGTCCCACTTGGGCTCCCGCAGAGAGTGGACACCTATCAGGGGGCTG 964
 |||||
 DB 241 GTGACTGTCCCACTTGGGCTCCCGCAGAGAGTGGACACCTATCAGGGGGCTG 300
 |||||

OY 965 ACCCATCTTGGCAGACGCTCCGCTCCGACCCCATCCCAACCCCTTCAGAGTGG 1024
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 DB 301 ACCCATCTTGGCAGACGCTCCGCTCCGACCCCATCCCAACCCCTTCAGAGTGG 360
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OY 1025 AGGACAGGCCCCACAAGCCACAGACCTAGACATGATACCCCGCAGCTTACGCG 1084
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 DB 361 AGGACAGGCCCCACAAGCCACAGACCTAGACATGATACCCCGCAGCTTACGCG 420
 |||||

OY 1085 TGTGTGGAAGAGTGGCCCCGTTGGCTGGAAGAAATGCTGGGGGCTTACGGCTGAGCG 1144
 |||||
 DB 421 TGTGTGGAAGAGTGGCCCCGTTGGCTGGAAGAAATGCTGGGGGCTTACGGCTGAGCG 480
 |||||

OY 1145 ACCAGAGATGATGAGTGGCTGAGCTGCAGAAAGGGGCTGCTGGCGAGGCGCAATACA 1204
 |||||
 DB 481 ACCAGAGATGATGAGTGGCTGAGCTGCAGAAAGGGGCTGCTGGCGAGGCGCAATACA 540
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OY 1205 GCATCTTGGCAGCTGGAAGGGGGCGCAGCGCGCGGCGAGGCCACGCTGAGCTGTGG 1264
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 DB 541 GCATCTTGGCAGCTGGAAGGGGGCGCAGCGCGCGGCGAGGCCACGCTGAGCTGTGG 600
 |||||

OY 1265 GAGCGGTCTCCGCGACATGACCTGCTGGGCTGCTGAGAGACATGAGAGGGGCTTT 1324
 |||||
 DB 601 GAGCGGTCTCCGCGACATGACCTGCTGGGCTGCTGAGAGACATGAGAGGGGCTTT 660
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OY 1325 GCGGCGCGCGCGCTCCCGCGCGCGCGCGAGCTTCTCAGATGA 1368
 |||||
 DB 661 GCGGCGCGCGCG-CTTCCGCGCGCGCGAGCTTCTCAGATGA 703
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RESULT 6
 AUI31978 761 bp mRNA linear EST 01-AUG-2002
 LOCUS AUI31978 NT2RP3 Homo sapiens cDNA clone NT2RP300370 5', mRNA
 DEFINITION
 ACCESSION AUI31978
 VERSION AUI31978.1 GI:10992332
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 761)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Isogai, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory

Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'-6 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source
 1. 761
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NT2RP300370"
 /clone_1bp="NT2RP3"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
 cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 178 a 199 c 201 g 179 t 4 others
 ORIGIN

Query Match 49.9%; Score 682.4; DB 9; Length 761;
 Best Local Similarity 99.1%; Pred. No. 6.1e-158;
 Matches 694; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

OY 1 ATGGGCTCTCTCCACCGTCCCTGACCTGCTGCTGCACCTGCTGCTGCTGCTGCTG 60
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 DB 62 ATGGGCTCTCTCCACCGTCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 121
 |||||

OY 61 GGAATATACCCCTCAGGGGTTATTGAGTGGTCCCTCAGCTTAGGGGACAGGAGAAAGA 120
 |||||
 DB 122 GGAATATACCCCTCAGGGGTTATTGAGTGGTCCCTCAGCTTAGGGGACAGGAGAAAGA 181
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OY 121 GATAGTGTGTGCCCAAGAAATATATCAACCTCAAAATTAATTCGATTTGCTGTAC 180
 |||||
 DB 182 GATAGTGTGTGCCCAAGAAATATATCAACCTCAAAATTAATTCGATTTGCTGTAC 241
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OY 181 AAGTCCCAAAAGAAAGAACTTCTTACATGACTTCCAGGCGCGGGCAGATATCGAG 240
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 DB 242 AAGTCCCAAAAGAAAGAACTTCTTACATGACTTCCAGGCGCGGGCAGATATCGAG 301
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OY 241 TGCAGGAGTGTGAGAGGGGCTCTTCAACGCTTCAGAAACCAACTCAGACACTGCTC 300
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 DB 302 TGCAGGAGTGTGAGAGGGGCTCTTCAACGCTTCAGAAACCAACTCAGACACTGCTC 361
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OY 301 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTTCTTGGACAGTGGAC 360
 |||||
 DB 362 AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGAATCTTCTTGGACAGTGGAC 421
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OY 361 CGGACACCGTGTGTGGCTGAGAGAAACAGTACCGGCAATTAATGGAGTGAAGAACTT 420
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 DB 422 CGGACACCGTGTGTGGCTGAGAGAAACAGTACCGGCAATTAATGGAGTGAAGAACTT 481
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OY 421 TTCCAGTCTTCAATTTGACGCTTGCCTCAATGGGAGCGTGCACCTCTCCGCGCAGAG 480
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 DB 482 TTCCAGTCTTCAATTTGACGCTTGCCTCAATGGGAGCGTGCACCTCTCCGCGCAGAG 541
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OY 481 AAACAGAACACCGTGTGACCTGCGCATGAGTTTCTTTAAGAGAAAGAGTGTGTC 540
 |||||
 DB 542 AAACAGAACACCGTGTGACCTGCGCATGAGTTTCTTTAAGAGAAAGAGTGTGTC 601
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OY 541 TCCTGTACTACTGTAAAGAAAGCTTGAAGTGCACGAAGTGTGCTTACCCAGATTGAG 600
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 DB 602 TCCTGTACTACTGTAAAGAAAGCTTGAAGTGCACGAAGTGTGCTTACCCAGATTGAG 661
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OY 601 AATGTTAAGGACACTGAGAGACTCAGGACACAGAGTC-TGTTGCCCTCGTCAATTTCTT 659
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 DB 662 AATGTTAAGGACACTGAGAGACTCAGGACACACAAAGCTTGTGTCCTCGGCAATTTCTT 721
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OY 660 TGTCTTTGCTTTTATCCCTCTCTTCATTTGATTGAG 699
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 DB 722 TGTCTTTGCTTTTATCCCTCTCTTCATTTGATTGAG 761
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[illegible]

Db	594	CGGAGACCGTGTGTGGCGTGCAGGAAAGAACCGTACCGGCATTATTGGAGTGAACACTT	653
QY	421	TTCCAGTGTCTTAATTGCAAGCCTCTGCTCAATTGGAGCCGTACACTTCTCTGCCAGAG	480
Db	654	TTCCAGTGTCTTAATTGCAAGCCTCTGCTCAATTGGAGCCGTACACTTCTCTGCCAGAG	713
QY	481	AAACGAACACCGTGTGCAACCTGCATGCAGG-TTTTCTTTAAAGAAAAGAGTGTGT	539
Db	714	AAACGAACACCGTGTGCAACCTGCATGCAGGTTTTCTTTCTTAAGAGAAAGAGTGTGT	773
QY	540	CTCTGTAGTAACCTGTAAGAAAAAGCTTGAGTGCAGCAAGTTGTCTTACCCAGATTGA	599
Db	774	CTCTGTAGTAACCTGTAAGAAAAAGCTTGAGTGCAGCAAGTTGTCTTACCCAGATTGA	832
QY	600	GAATGTAAAGGCACTGAGGAGTCAAGGCAACCACTGCTGTCGCCCTGATTTCTT	659
Db	833	GAATGTAAAGGCACTGAGGAGTCAAGGCAACCACTGCTGTCGCCCTGATTTCTT	892
QY	660	TGCTGTGGCTTTTATCCCTCTCTTATCTGTTAATGTTATGATCGCTACC	709
Db	893	TGCTGTGGCTTTTATCTCTCTCTTATCTGTTAATGTTATGATCGCTACC	942
RESULT 8			
BM546826		1070 bp	linear EST 20-FEB-2002
LOCUS			
DEFINITION	AGNCOURT 6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723557		
LOCUS	5', mRNA sequence.		
ACCESSION	BM546826		
VERSION	BM546826.1	GI:18780096	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LML at: http://image.lnl.gov Plate: L1AM12711 row: g column: 14 High quality sequence start: 2 High quality sequence stop: 669. Location/Qualifiers 1. 1070 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5723557" /clone_id="NIH_MGC_125" /lab_host="DH10B" /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; site:1: EcoRV (destroyed); site:2: NotI; RNA source pool from 49 females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1.3-5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."		
FEATURES			
source			
BASE COUNT	241 a	311 c	293 g 224 t 1 others
ORIGIN			
Query Match	49.7%	Score 679.8;	DB 13; Length 1070;
Best Local Similarity	94.0%	Pred. No. 2.8e-157;	

Matches 741: Conservative 0: Mismatches 38: Indels 9: Gaps 3:									
OY	1	ATGGGACCTCTCCACCGTCTGACCTGCTGCTGCCACTGTGTCTCTGGAGCTGTGGTG	60						
Db	206	ATGGGACCTCTCCACCGTCTGACCTGCTGCTGCCACTGTGTCTCTGGAGCTGTGGTG	265						
OY	61	GGAAATATACCCCTCAGGGGTTATTGGACTGTGTCCTCACCCTTACGGGAGACAGGAGAAGA	120						
Db	266	GGAAATATACCCCTCAGGGGTTATTGGACTGTGTCCTCACCCTTACGGGAGACAGGAGAAGA	325						
OY	121	GATAGTGTGTGTCCCAAGGAAATATATATCCACCTCAAAATATATTCGATTTGCTGTACC	180						
Db	326	GATAGTGTGTGTCCCAAGGAAATATATATCCACCTCAAAATATATTCGATTTGCTGTACC	385						
OY	181	AAGTGGCACAAGGAACCTACTGTATGACATGTGTCCAGGCGCGGGAGAGATACGGAC	240						
Db	386	AAGTGGCACAAGGAACCTACTGTATGACATGTGTCCAGGCGCGGGAGAGATACGGAC	445						
OY	241	TGCAGGAGTGTGAGAGCGGCTCTTACACCGCTTACAGAAACACCACTCAGACACTGCCCTC	300						
Db	446	TGCAGGAGTGTGAGAGCGGCTCTTACACCGCTTACAGAAACACCACTCAGACACTGCCCTC	505						
OY	301	AGCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGTGAGATCTCTTCTTGACACAGTGAC	360						
Db	506	AGCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGTGAGATCTCTTCTTGACACAGTGAC	565						
OY	361	CGGGACACCGTGTGTGGCTGCGAGAAACCACTACCGGCAATATTTGAGTGAAACCTT	420						
Db	566	CGGGACACCGTGTGTGGCTGCGAGAAACCACTACCGGCAATATTTGAGTGAAACCTT	625						
OY	421	TTCCAGTGTCTCAATTTGACGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG	480						
Db	626	TTCCAGTGTCTCAATTTGACGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG	685						
OY	481	AAACAGAACACCGTGTGCACCTGCCATGCAAGTCTTCTTAAAGAGAAAAAGATGTGTC	540						
Db	686	AAACAGAACACCGTGTGCACCTGCCATGCAAGTCTTCTTAAAGAGAAAAAGATGTGTC	745						
OY	541	TCCTGTAGTAACTGTAAAGAAACCGTGSATGTCACGAATTTGGCTTACCCAGATTTAG	600						
Db	746	TCCTGTAGTAACTGTAAAGAAACCGTGSATGTCACGAATTTGGCTTACCCAGATTTAG	805						
OY	601	AATGTTAAGGCACTGAGAGACTCAGGACACACAGTGTCTTG-CGCCCTGCTATTCTT	659						
Db	806	AATGTTAAGGCACTGAGAGACTCAGGACACACAGTGTCTTG-CGCCCTGCTATTCTT	865						
OY	660	TGGCTTTGCTTTTATTCCTCTCTTCAATGTTTAAATGATCGCTACCAAC--GTTGG	717						
Db	866	TGGCTTTGCTTTTATTCCTCTCTTCAATGTTTAAATGATCGCTACCAAC--GTTGG	925						
OY	718	AAGTCCAAAG-----CTCTACTCATGTGTTTGGGAAATCGACACCTGAAAAAGGGG	771						
Db	926	AAGTCCCAAGGCTCTACCTCTTGGTTTGGGGGGGAATTCGACACACCTGAAAAAGAGG	985						
OY	772	GAGCTTGA 779							
Db	986	GGGGAAGA 993							
RESULT 9									
LOCUS	AL577008	975 bp	mRNA	linear	EST 16-FEB-2001				
DEFINITION	AL577008	LT1_NFL006.PL2	Homo sapiens	cdna clone CS0D1082YA01 5					
ACCESSION	AL577008	LT1_NFL006	prtm, mRNA sequence.						
VERSION	AL577008.1	GI:12939716							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.								

TITLE									
JOURNAL									
COMMENT									
Full-length cDNA libraries and normalization									
Unpublished (2001)									
Contact: Genoscope									
Genoscope - Centre National de Sequencage									
BP 191 91006 Evry cedex - France									
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.									
FEATURES									
source									
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/db_xref="taxon:9606"									
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/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA									
was primed with a NotI-oligo(dT) primer. Five prime end									
enriched, double-stranded cDNA was digested with Not I and									
cloned into the Not I and Eco RV sites of the pCMVSPORT 6									
vector. Library was normalized. Library was constructed by									
Life Technologies. Contact : Peng Liang Life Technologies,									
a division of Invitrogen 9800 Medical Center Drive									
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371									
Email : filiang@life.com									
http://fulllength.invitrogen.com"									
BASE COUNT									
231 a 258 c 259 g 221 t 6 others									
ORIGIN									
Query Match									
Best Local Similarity 97.9% Pred. No. 6.9e-157;									
Matches 704: Conservative 4: Mismatches 8: Indels 3: Gaps 2:									
OY	1	ATGGGACCTCTCCACCGCTGACCTGCGTGCACAGTGTGCTCTGAGAGCTGTGGTG	60						
Db	256	ATGGGACCTCTCCACCGCTGACCTGCGTGCACAGTGTGCTCTGAGAGCTGTGGTG	315						
OY	61	GGAATATATACCCCTCAGGGGTTATTTGACTGTCCCTCACCCTTACGGGAGACAGGAGAAGA	120						
Db	316	GGAATATATACCCCTCAGGGGTTATTTGACTGTCCCTCACCCTTACGGGAGACAGGAGAAGA	375						
OY	121	GATAGTGTGTGTCCCAAGGAAATATATATACACCTCAAAATATATTCATTTGCTGTACC	180						
Db	376	GATAGTGTGTGTCCCAAGGAAATATATATACACCTCAAAATATATTCATTTGCTGTACC	435						
OY	181	AAGTGGCACAAGGAACCTACTGTATACATGACTGTCCAGGCGCGGGAGAGATACGGAC	240						
Db	436	AAGTGGCACAAGGAACCTACTGTATACATGACTGTCCAGGCGCGGGAGAGATACGGAC	495						
OY	241	TGCAGGAGTGTGAGAGCGGCTCTTACACCGCTTACAGAAACCACTCAGACACTGCCCTC	300						
Db	496	TGCAGGAGTGTGAGAGCGGCTCTTACACCGCTTACAGAAACCACTCAGACACTGCCCTC	555						
OY	301	ACCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGTGAGATCTCTTTCGACAGTGGAC	360						
Db	556	ACCTGCTCCAAATGCCGAAAGAAATGGGTACAGTGTGAGATCTCTTTCGACAGTGGAC	615						
OY	361	CGGGACACCGTGTGTGGCTGCGAGAAACCACTACCGGCAATATTTGAGTGAAAACTT	420						
Db	616	CGGGACACCGTGTGTGGCTGCGAGAAACCACTACCGGCAATATTTGAGTGAAAACTT	675						
OY	421	TTCCAGTGTCTCAATTTGACGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG	480						
Db	676	TTCCAGTGTCTCAATTTGACGCTTGCCTCAATGGGACCGTGCACCTCTCTGCCAGAG	735						
OY	481	AAACAGAACACCGTGTGCACCTGCCATGCAAGTCTTCTTAAAGAGAAAAAGATGTGTC	540						
Db	736	AAACAGAACACCGTGTGCACCTGCCATGCAAGTCTTCTTAAAGAGAAAAAGATGTGTC	795						
OY	541	TCCTGTAGTAACTGTAAAGAAAGCGTGAAGTGCAGCAAGTTG-TGGCTACCCAGATTGA	599						
Db	796	TCCTGTAGTAACTGTAAAGAAAGCGTGAAGTGCAGCAAGTTG-TGGCTACCCAGATTGA	855						
OY	600	GAATGTTAAGGGCACTGAGAGACTCAGGACACCACTGCTGTTGCCCTGTGCTATTCTT	659						
Db	856	GAATGTTAAGGGCACTGAGAGACTCAGGACACCACTGCTGTTGCCCTGTGCTATTCTT	915						

Qy	660	TGCTGTTGGCCCTTATATCCCTCTCTGATATGCTTAATGATGCGCTTACCAAGCGGTGA	718
Db	916	TGCTGTTGGCCCTT--ATCCCCCTCTTATGCTTAAATGATATCGCTACCAAGGTGAA	972
RESULT	10		
LOCUS	BM742388	669 bp	linear
DEFINITION	K-EST0015256 S6SNU620 Homo sapiens CDNA clone S6SNU620-5-C12 5'		
ACCESSION	BM742388		
VERSION	BM742388.1	GI:19063703	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 669) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.		
TITLE	21C Frontier Korean EST project 2001		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 5 row: C column: 12 High quality sequence stop: 669. Location/Qualifiers 1. 669 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="S6SNU620-5-C12" /clone_1lb="S6SNU620" /sex="F" /tissue_type="Ascites" /cell_type="Scattering floating" /cell_line="SNU-620" /lab_host="Top10F/" /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."		
BASE COUNT	128 a 239 c 193 g 109 t		
ORIGIN			
Query Match	48.9%	Score 669;	DB 14; Length 669;
Best Local Similarity	100.0%	Pred. No. 1,2e-154;	
Matches 669;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	688	ATTGGTTTAATGATATCGCTACCAAGCGGTGAAGTCACAGCTCTACTCATTTGTTGTGGG	747
Db	1	ATTGGTTTAATGATATCGCTACCAAGCGGTGAAGTCACAGCTCTACTCATTTGTTGTGGG	60
Yy	748	AAATGACACCTGAAAAAGAGGGGAGCTTGAAGGAACCTACTACTAAGCCCTG6GCCCA	807

Db	61	AAATGACACCTGAAAAAGAGGGGGAGCTTGAAGGAACACTAATCAATGAAGCCCTGGGCCCA	120		
QY	808	AAACCAAGCTTAGTCCCACTCCAGGCTTACACCCACCCTGGGCTTCAAGTCCCGTGCC	867		
Db	121	AAACCAAGCTTCAATCCCACTCCAGGCTTACACCCACCCTGGGCTTCAAGTCCCGTGCC	180		
QY	868	AGTTCACCTTACCTCCGAGCTCCACCTTATACCCCGGAGCTGTCACCAGTTTGGGGCT	927		
Db	181	AGTTCCACCTTACCTCCGAGCTCCACCTTATACCCCGGAGCTGTCACCAGTTTGGGGCT	240		
QY	928	CCCCGAGAGAGTGGACACACCCCTATACGAGGGGGGTGACCCCATCTTTCGACAGCCCTC	987		
Db	241	CCCCGAGAGAGTGGACACACCCCTATACGAGGGGGGTGACCCCATCTTTCGACAGCCCTC	300		
QY	988	GCCTCCGACCCCATCCCAACCCCTTTAGAGAGTGGGAGAGACAGGGCCACAAAGCCACAG	1047		
Db	301	GCCTCCGACCCCATCCCAACCCCTTTAGAGAGTGGGAGAGACAGGGCCACAAAGCCACAG	360		
QY	1048	AGCCTAGACACTGATGACCCCGCGACGCGTATACGCGGTGGAGAACTGCCCCCGTTG	1107		
Db	361	AGCCTAGACACTGATGACCCCGCGACGCGTATACGCGGTGGAGAACTGCCCCCGTTG	420		
QY	1108	CGCTGGAAGGAATTTGTCGCGGCGCTAGGGCTGACGACACAGAGATGATCGGCTGGAG	1167		
Db	421	CGCTGGAAGGAATTTGTCGCGGCGCTAGGGCTGACGACACAGAGATGATCGGCTGGAG	480		
QY	1168	CTGCAGAACGGGGCGCTGCTGCGGCGAGGCGCAATATACAGATCTGGCGACTGGAGGCGG	1227		
Db	481	CTGCAGAACGGGGCGCTGCTGCGGCGAGGCGCAATATACAGATCTGGCGACTGGAGGCGG	540		
QY	1228	CGCACGCGCGCGGCGGAGGCGCACGCTGGAGCTGTGGAGCGGCTCTCGCGACATGAGAC	1287		
Db	541	CGCACGCGCGCGGCGGAGGCGCACGCTGGAGCTGTGGAGCGGCTCTCGCGACATGAGAC	600		
QY	1288	CTGCTGGGCTGCTGGAGACATGAGAGAGCGCTTTGGGCGCCCGCGCCTCCCGGCC	1347		
Db	601	CTGCTGGGCTGCTGGAGACATGAGAGAGCGCGCTTTGGGCGCCCGCGCCTCCCGGCC	660		
QY	1348	GCGGCCAGT 1356			
Db	661	GCGGCCAGT 669			
RESULT 11					
LOCUS	BG180101	974 bp	mRNA linear EST 06-FEB-2001		
DEFINITION	60232676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5', mRNA sequence.				
ACCESSION	BG180101				
VERSION	BG180101.1	GI:12686804			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 974)				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapds-remail.nih.gov				
	Tissue Procurement: DCTD/DTF				
	cDNA Library Preparation: Life Technologies, Inc.				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LLAM10185 row: g column: 20				
	High quality sequence stop: 657.				
FEATURES	Location/Qualifiers				
source	1..974				
	/organism="Homo sapiens"				

[illegible]

FEATURES	Source
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DEFINITION	BG680679 718 bp mRNA linear EST 01-MAY-2001
ACCESSION	602626956F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751536 5',
VERSION	BG680679
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Hominiidae; Homo.
TITLE	1 (bases 1 to 718)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: James Cleaver, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LLM10608 row: b column: 17 High quality sequence stop: 679. Location/Qualifiers 1. 718 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4751536" /clone_lib="NCI_CGAP_Skn4" /tissue_type="squamous cell carcinoma" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: oligo dT. Average insert size 1.5kb. Library constructed by Life

BASE COUNT	134 a	254 c	198 g	132 t	
ORIGIN	Technologies. Note: this is a NCI_CGAP Library."				
Query Match	48.8%; Score 667; DB 12; Length 718;				
Best Local Similarity	98.4%; Pred. No. 3,8e-154;				
Matches 684; Conservative	0; Mismatches 10; Indels 1; Gaps 1				
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OY	714	GTGGAAGTCCAGAGCTCTACTCATCTGTTTGTGGAAATGACACCTGAAAGAGAGGGGA	773		
DB	61	GTGGAAGTCCAGAGCTCTACTCATCTGTTTGTGGAAATGACACCTGAAAGAGAGGGGA	120		
OY	774	GCTTAAGAGAACTACTACTAAGCCCCCTGGCCCCCAACCCAAAGCTTCAGTCCACTTCAGG	833		
DB	121	GCTTAAGAGAACTACTACTAAGCCCCCTGGCCCCCAACCCAAAGCTTCAGTCCACTTCAGG	180		
OY	834	CTTCAACCCCCACCCCTGGGCTTCAGTCCGCTGCCAGTTCCACCTTCACCTCCAGCTCCAC	893		
DB	181	CTTCAACCCCCACCCCTGGGCTTCAGTCCGCTGCCAGTTCCACCTTCACCTCCAGCTCCAC	240		
OY	894	CTATACCCCCGCTGAGCTGTCGCCAATTTTGGGCTCCCCGAGAGAGTGGGACACCAACCTA	953		
DB	241	CTATACCCCCGCTGAGCTGTCGCCAATTTTGGGCTCCCCGAGAGAGTGGGACACCAACCTA	300		
OY	954	TCAGGGGGCTGACCCCATCTTGCACAGACCTTCGCTCCGACCCCATCCCAACCCCTT	1013		
DB	301	TCAGGGGGGGTACCCCATCTTGCACAGACCTTCGCTCCGACCCCATCCCAATCCCTT	360		
OY	1014	TCAGAGTGGGAGAGACAGCGCCACAGACCCACAGAGCTTAGACACTGATGACCCCGGAC	1073		
DB	361	TCAGAGTGGGAGAGACAGCGCCACAGACCCACAGAGCTTAGACACTGATGACCCCGGAC	420		
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DB	421	GCTGTACCCCGCTGAGGAGAAAGCTCCCCCTTGGGCTGGAGAAATTCGTGCGGCGCT	480		
OY	1134	AGGCGTGAAGCAGACACAGAGATGATCGGCTGGAGCTGAGAAAGGAGGCTGCTCCGGA	1193		
DB	481	AGGCGTGAAGCAGACACAGAGATGATCGGCTGGAGCTGAGAAAGGAGGCTGCTCCGGA	540		
OY	1194	GCGCGAATATACAGCATGTGGGCGACCTGGAGGCGGCGACGCGGCGGCGAGGACCAAGCT	1253		
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DB	601	GGAGTCTGTGGGAGCGCGTGTCCGGGAATATGACCTGCTGGGCTTCCTGTGGAGGACATCG	660		
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DB	661	AGGAGGCGCTTGTGGGCGCCCGCGCGCTCCCGCCG 695			
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LOCUS	AGENCOURT_6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041				
DEFINITION	5', mRNA sequence.				
ACCESSION	BM800044				
VERSION	BM800044.1 GI:19116867				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
TITLE	NIH-MGC http://mgi.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				


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Db 498 AGCTGCTCCAAATGCCGAAAGAAATGGTCCAGGTGGAGATCTTCTTTCACAGTGGAC 557
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Search completed: December 4, 2002, 21:42:31
 Job time : 2087 secs

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Qy 121 GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATTAATTCATTGTGTATCC 180
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Db 976 TCCAGCTCTACTCCATTTGTTGAGAAATGCACACCTGAAAAAGAGGGGAGCTTGA 1035
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US-09-505-250-3

; Sequence 3, Application US/09505250A

; Patent No. 6329148

; GENERAL INFORMATION:

; APPLICANT: Rosen, Glenn

; APPLICANT: Kao, Peter

; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with

; FILE REFERENCE: SUN-109PRV2

; CURRENT FILING DATE: 2000-02-15

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 2161

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (256)...(1623)

US-09-505-250-3

Query Match

Best Local Similarity 99.9%; Score 1366.4; DB 4; Length 2161;

Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1576 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623
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RESULT 3
US-08-321-668-1
Sequence 1, Application US/08321668
Patent No. 565859
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEY, Eugene
APPLICANT: BARKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
THE TMR RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321.668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
US-08-321-668-1
Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 4 US-08-837-941-1

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; Sequence 1, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFLOMEY, Eugene
; APPLICANT: BARKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

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; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROMDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,668
; FILING DATE: 12-OCT-1994
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROMDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-837-941-1

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Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGGCTCTTCACCGTGCCTGACCTGTCTGTGCACCTGTGTCTCTGTGAGCTGTGTGCTG 60
Db 256 ATGGGCTCTTCACCGTGCCTGACCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 315
QY 61 GGAATATATACCCCTCAGGGGTTATTGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 316 GGAATATATACCCCTCAGGGGTTATTGGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 375
QY 121 GATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 376 GATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 435
QY 181 AAGTGCACAAAGAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 436 AAGTGCACAAAGAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 495
QY 241 TGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 496 TGCAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 555
QY 301 AGCTGTCCAAATGCGCAAGAAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 556 AGCTGTCCAAATGCGCAAGAAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 615
QY 361 CGGAGACACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420

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Db 616 CGGACACCGTGTGTGCTGCGAGAGAACCAAGTACCGGATTTATTTGGAGTGAATAACCTT 675
 Oy 421 TTCCAGTCTTCAATTTGACAGCTCTGCTCAATGGAGCCGTGACACTTCTCTGCCAGAG 480
 Db 676 TTCCAGTCTTCAATTTGACAGCTCTGCTCAATGGAGCCGTGACACTTCTCTGCCAGAG 735
 Oy 481 AAACGACACCGTGTGACAGCTCTGCTCAATGGAGCCGTGACACTTCTCTGCCAGAG 540
 Db 736 AAACGACACCGTGTGACAGCTCTGCTCAATGGAGCCGTGACACTTCTCTGCCAGAG 795
 Oy 541 TCCTGTAGTAACTGTAGAAAAAGCTGAGTGCACAGAAATTTGCTTACCCAGATTTAG 600
 Db 796 TCCTGTAGTAACTGTAGAAAAAGCTGAGTGCACAGAAATTTGCTTACCCAGATTTAG 855
 Oy 601 AATGTTAAGGGCAGTGAAGAGTGCACAGAAATTTGCTTACCCAGATTTAG 660
 Db 856 AATGTTAAGGGCAGTGAAGAGTGCACAGAAATTTGCTTACCCAGATTTAG 915
 Oy 661 GGTCTTGTGCTTATTTCCCTCTCTTCAATTTGCTTACCCAGATTTAG 720
 Db 916 GGTCTTGTGCTTATTTCCCTCTCTTCAATTTGCTTACCCAGATTTAG 975
 Oy 721 TCACAGTCTTACTCCATTTGTTGGAATTCGACACCTGAAAGAGGGGAGCTTGA 780
 Db 976 TCACAGTCTTACTCCATTTGTTGGAATTCGACACCTGAAAGAGGGGAGCTTGA 1035
 Oy 781 GGAATCTACTACTAGCCCTTGGCCCAACCAAGCTTCACTTCCAGTTCAGCTTCAAC 840
 Db 1036 GGAATCTACTACTAGCCCTTGGCCCAACCAAGCTTCACTTCCAGTTCAGCTTCAAC 1095
 Oy 841 CCCACCTTGGGGTGTAGTCCGCTGCGCAGTTCCACCTTCACTTCCAGTTCAGCTTCAAC 900
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 Oy 901 CCCGCTGACTGTCCCACTTTTCCGCTCCCGCAGAGAGTGGCACCACCTATCAGGGG 960
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 Db 1216 GCTGACCCCATCTTGGCAGACCTCTGCTCCGACCCCATCTCCCAACCCCTTCAAGAG 1275
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 Db 1276 TGGGAGAGAGGCGCCACAGGACAGAGCCTAGACACTGAGTACCCGCGAGCTGTAC 1335
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 Db 1336 GCCGTGTGTGAGAAAGTGTGCGCTTGGCTGGAAGAAATTCGTGCGGCGCTTAGGGCTG 1395
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 Db 1456 TACACAGATGTGTGAGAGTGTGAGAGGGGCGACGCGCGCGGAGGACCAAGTGTGAGCTG 1515
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 Db 1516 CTGGAGACCTGTCTCGGAGACATGTGAGTGTGCTGCTGCTGAGAGATCGAGAGGCG 1575
 Oy 1321 CTTTGGGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGAGTCTTTCAGATGA 1368
 Db 1576 CTTTGGGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGAGTCTTTCAGATGA 1623

: APPLICANT: NOPHAR, YARON
 : APPLICANT: KEMPER, OLIVER
 : APPLICANT: ENGELMANN, HARTMUT
 : APPLICANT: BRAKEBUSCH, CORD
 : APPLICANT: ADERKA, DAN
 : TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
 : TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
 : NUMBER OF SEQUENCES: 26
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Browdy and Neimark
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/126,016
 : FILING DATE: 24-SEP-1993
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/625668
 : FILING DATE: 13-DEC-1990
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BROWDY, ROGER L.
 : REGISTRATION NUMBER: 25,618
 : REFERENCE/DOCKET NUMBER: WALLACH4
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-737-3528
 : TELEX: 248633
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2175 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 236..1620
 : FEATURE:
 : NAME/KEY: mat_peptide
 : LOCATION: 319..1620
 : US-08-126-016-1
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 : Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
 : Best Local Similarity 99.9%; Pred. No. 0;
 : Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ATGGGCGCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 Db 236 ATGGGCGCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
 Oy 61 GGAATATACCCCTCAGGGGTTATTGACTGTGCTTCACTTCACTTCACTTCACTTCACTTCA 120
 Db 316 GGAATATACCCCTCAGGGGTTATTGACTGTGCTTCACTTCACTTCACTTCACTTCACTTCA 375
 Oy 121 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATATATGATTTGCTGTAC 180
 Db 376 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATATATGATTTGCTGTAC 435
 Oy 181 AAGTCCCAAAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCGCGGCGAGAGATCGGAG 240
 Db 436 AAGTCCCAAAAGAAAGAACTACTTGTACAAATGACTGTCCAGGCGCGGCGAGAGATCGGAG 495
 Oy 241 TGCAGGAGAGTGTGAGAGGCGCTCTTCACTGCTTCACTGAGAAACCACTCAGACACTGCTC 300
 Db 496 TGCAGGAGAGTGTGAGAGGCGCTCTTCACTGCTTCACTGAGAAACCACTCAGACACTGCTC 555

RESULT 5
 US-08-126-016-1
 : Sequence 1, Application US/08126016
 : Patent No. 5811261
 : GENERAL INFORMATION:
 : APPLICANT: WALLACH, DAVID

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QY 301 AGCTGCTCAAATGCCGAAAGAAATGGGTGAGATCTCTTTCGACAGTGGAC 360
DB 556 AGCTGCTCAAATGCCGAAAGAAATGGGTGAGATCTCTTTCGACAGTGGAC 615
QY 361 CGGACACCGGTGTGGCTGAGAGAGAACAGTACCGGCAATTTGGAGTGAACCTT 420
DB 616 CGGACACCGGTGTGGCTGAGAGAGAACAGTACCGGCAATTTGGAGTGAACCTT 675
QY 421 TTCAGTGTCTCAATTCAGAGCTTGGCTCAATGGGACCGGCACTCTCTGACAGAG 480
DB 676 TTCAGTGTCTCAATTCAGAGCTTGGCTCAATGGGACCGGCACTCTCTGACAGAG 735
QY 481 AAACAGAACACCGGTGTGACACCTGACAGTGTCTTCTTAAGAGAAACAGATGTCT 540
DB 736 AAACAGAACACCGGTGTGACACCTGACAGTGTCTTCTTAAGAGAAACAGATGTCT 795
QY 541 TCCGTGTGTAATCTTAAGAAAGAGCTGAGTGCAGAAATGTTGCTTACCCAGATTGAG 600
DB 796 TCCGTGTGTAATCTTAAGAAAGAGCTGAGTGCAGAAATGTTGCTTACCCAGATTGAG 855
QY 601 AATGTAAAGGCACTGAGAGACTGAGGACCAAGTGTGTTGCCCTGGTCAATTTCTT 660
DB 856 AATGTAAAGGCACTGAGAGACTGAGGACCAAGTGTGTTGCCCTGGTCAATTTCTT 915
QY 661 GGTCTTGTGCTTTTATCCCTCTCTCTTCAATTTGTTAATGATGCTACCAAGGTGAG 720
DB 916 GGTCTTGTGCTTTTATCCCTCTCTCTCTTCAATTTGTTAATGATGCTACCAAGGTGAG 975
QY 722 TCCAAAGTCTACACCTCAATTTGTTGGGAAATCCGACACCTGAAAGAGGGGAGCTTGA 780
DB 976 TCCAAAGTCTACACCTCAATTTGTTGGGAAATCCGACACCTGAAAGAGGGGAGCTTGA 1035
QY 781 GGAACCTACTTAAGCCCTGAGCCCAACCAAGCTTACAGTCCACCTCCAGGCTTACC 840
DB 1036 GGAACCTACTTAAGCCCTGAGCCCAACCAAGCTTACAGTCCACCTCCAGGCTTACC 1095
QY 841 CCCACCTGAGGCTTCACTCCGTCGCCAGTTCACCTTCACTCCAGCTCCACCTATACC 900
DB 1096 CCCACCTGAGGCTTCACTCCGTCGCCAGTTCACCTTCACTCCAGCTCCACCTATACC 1155
QY 901 CCCGATGATCTGCCCACTTTGGGGCTCCCGGACAGAGAGTGGGACCACTTACAGGG 960
DB 1156 CCCGATGATCTGCCCACTTTGGGGCTCCCGGACAGAGAGTGGGACCACTTACAGGG 1215
QY 961 GCTGACCCCACTTGGGACAGCCCTGCTCCGACCCCACTCCCAACCCCTTACAGAG 1020
DB 1216 GCTGACCCCACTTGGGACAGCCCTGCTCCGACCCCACTCCCAACCCCTTACAGAG 1275
QY 1021 TGGAGAGACAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGGACGCTGTAC 1080
DB 1276 TGGAGAGACAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGGACGCTGTAC 1335
QY 1081 GCCGTGTGAGAGAACTGCCCCCGTTCGCTGGAAGGAATTCGTGGGGCGCTTAGGGCTG 1140
DB 1336 GCCGTGTGAGAGAACTGCCCCCGTTCGCTGGAAGGAATTCGTGGGGCGCTTAGGGCTG 1395
QY 1141 AGCAGACAGAGATCGATCGGCTGAGACTCAGAAACGGGCGCTGCTGGCGAGAGCCAA 1200
DB 1396 AGCAGACAGAGATCGATCGGCTGAGACTCAGAAACGGGCGCTGCTGGCGAGAGCCAA 1455
QY 1201 TACAGATGCTGAGGACCTGAGAGCGGACGACCGCGGCGGAGGACGCTGAGACTG 1260
DB 1456 TACAGATGCTGAGGACCTGAGAGCGGACGACCGCGGCGGAGGACGCTGAGACTG 1515
QY 1261 CTGGGAGAGCTGCTCCGCGACATGAGACTCTGCGCTGCTGAGAGACATGAGAGGCG 1320
DB 1516 CTGGGAGAGCTGCTCCGCGACATGAGACTCTGCGCTGCTGAGAGACATGAGAGGCG 1575
QY 1321 CTTTGGGAGCGCGCGGCTTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1368
DB 1576 CTTTGGGAGCGCGCGGCTTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1623

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RESULT 6
US-08-054-970-1
; Sequence 1, Application us/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W.
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-054-970-1

Query Match 99.9%; Score 1366.4; DB 4; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCTTCACCGGTGCTGACCTGCTGCTGCACTGGTGGCTCGAGAGCTGTTGGTG 60
DB 256 ATGGGCTCTTCACCGGTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
QY 61 GGAATATATCCCTTCAGGGGTTATTGAGCTGTGCTTCACTAGGGGACAGGAGAAAGAGA 120
DB 316 GGAATATATCCCTTCAGGGGTTATTGAGCTGTGCTTCACTAGGGGACAGGAGAAAGAGA 375
QY 121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAATAATATGATTTGCTGTACC 180
DB 376 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAATAATATGATTTGCTGTACC 435
QY 181 AAGTGCACAAAGAACCTTGTACATGACTGTGTCAGAGCCCGGGGACAGATTAAGAGAC 240
DB 436 AAGTGCACAAAGAACCTTGTACATGACTGTGTCAGAGCCCGGGGACAGATTAAGAGAC 495
QY 241 TGCAGGAGATGTAGAGAGCGCTCTTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 300
DB 496 TGCAGGAGATGTAGAGAGCGCTCTTTCACCGCTTCAGAAAAACACCTCAGACACTGCTC 555
QY 301 AGCTGCTCAAATGCCGAAAGAAATGGGTGAGATCTCTTTCGACAGTGGAC 360
DB 556 AGCTGCTCAAATGCCGAAAGAAATGGGTGAGATCTCTTTCGACAGTGGAC 615

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Oy	361	CGGACACCGCTGTGTGGCTGTGACAGAAAGAACACGATACCGGCATTTATTTGGAGTGGAAACCTT	420
Db	616	CGGGACACCGCTGTGTGGCTGTGACAGAAAGAACACGATACCGGCATTTATTTGGAGTGGAAACCTT	675
Oy	421	TTTCAGAGCTTCAATTTGACGCTCTGCTCAATTTGGAGACGTCGACCTCTCTGCGCAGAG	480
Db	676	TTTCAGAGCTTCAATTTGACGCTCTGCTCAATTTGGAGACGTCGACCTCTCTGCGCAGAG	735
Oy	481	AAACAGAACACCGTGTGACACCTGCGCATGTGACAGGTTTCTTTCTTAAGAGAAACGAGTGTG	540
Db	736	AAACAGAACACCGTGTGACACCTGCGCATGTGACAGGTTTCTTTCTTAAGAGAAACGAGTGTG	795
Oy	541	TTCTCTGTACTAATCTTAAGAAAACCTCGAGATGACAGAAATTTGGCTTACCCACATTTAG	600
Db	796	TTCTCTGTGTAACTGTAAAGAAAACCTCGAGATGACAGAAATTTGGCTTACCCACATTTAG	855
Oy	601	AATTTTAAGGACACTGAGACATGAGCACACAGTACCTTTGCCCCCTGATCTTCTTTCTTT	660
Db	856	AATTTTAAGGACACTGAGAGACTGAGACATGAGCACACAGTACCTTTGCCCCCTGATCTTCTTTCTTT	915
Oy	661	GCTCTTTGCCCTTTTATCCCTCTCTTCAATTTGTTTAAATGTATGCTTACCAACGGTGGAG	720
Db	916	GCTCTTTGCCCTTTTATCCCTCTCTTCAATTTGTTTAAATGTATGCTTACCAACGGTGGAG	975
Oy	721	TTCCAAAGCTACTACCTCATTGTTTGTGGGAAATGACACCTGAAAGAGGGGAGACTTGA	780
Db	976	TTCCAAAGCTACTACCTCATTGTTTGTGGGAAATGACACCTGAAAGAGGGGAGACTTGA	1035
Oy	781	GGAACTACTACTAAGCCCTCGGCCCAAAACCCAAAGCTTATGATCCCACTCAGGCTTCAAC	840
Db	1036	GGAACTACTACTAAGCCCTCGGCCCAAAACCCAAAGCTTATGATCCCACTCAGGCTTCAAC	1095
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Oy	901	CCGGGTGACTGTGCCCACTTTGGGGGTCGCCGAGAGAGATGGAGCAACCCATATCAGGG	960
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Oy	1081	GCCGGGTGGAGAAACGAGCCCGCGTTGGCGTGGAAAGAAATTTGATGGGGGCGCTTAGGGTG	1140
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Db	1456	TACAGCATGTGTGGGACCTTGGAGGCGGCGACGCGCGCGCGGCGAGAGCCACGCTGGAGCTG	1515
Oy	1261	CTGGGACGCGTGTCTCCCGACATGTGACCTTTGGGCTGTGCTGGAGACATCGAGAGCGG	1320
Db	1516	CTGGGACGCGTGTCTCCCGACATGTGACCTTTGGGCTGTGCTGGAGACATCGAGAGCGG	1575
Oy	1321	CTTTTGGGGGCGCGCGCGCTTCCGCGCGCGCGCGCCACGTTCTTCTAGATGA	138
Db	1576	CTTTTGGGGGCGCGCGCGCTTCCGCGCGCGCGCGCCACGTTCTTCTAGATGA	1623

421 TTCAGAGCTTCATTAATGACAGCTTGCCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 480
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575 TTCAGAGCTTCATTAATGACAGCTTGCCTCAATGGAGCCGTGCACCTCTCTGCCAGAG 634
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481 AAACAGAACACCGGTGACAGCTGCACATGCAAGGTTTCTTTCTAAGAAAAAGAGTGTGC 540
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901 CCCGGTGAAGTGTCCCAAGCTTTGCGGCTCCCGCAGAGAGAGTGTGACACCTTATCAGGG 960
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1115 GGTGAGCCCATCTTGGCAGACAGCCCTGCGCTCCGACCCCATCCCAAGCCCTTCAAGAG 1174
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1021 TGGGAGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
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1175 TGGGAGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1234
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1081 GCGGTGTGTGAGAAAGTGTGCGCTGGGCTGGAAGAAATTTGCTGCGGCGCTTACGGCTG 1140
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1235 GCGGTGTGTGAGAAAGTGTGCGCTGGGCTGGAAGAAATTTGCTGCGGCGCTTACGGCTG 1294
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1141 AGCGACACAGAGATGATGAGTGTGAGAGTGCAGAAAGGAGGAGGAGGAGGAGGAGGAGG 1200
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1295 AGCGACACAGAGATGATGAGTGTGAGAGTGCAGAAAGGAGGAGGAGGAGGAGGAGGAGG 1354
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1201 TACAGCATGCTGGCAGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
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1261 CTGGGAGCGGTGCTCTCCGCGACATGACCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCT 1320
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1415 CTGGGAGCGGTGCTCTCCGCGACATGACCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCT 1474
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1475 CTTTGGCGCGCGCGCGCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522
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RESULT 9
US-08-762-308-10
; Sequence 10, Application US/08762308
; Patent No. 5925548
; GENERAL INFORMATION:
; APPLICANT: Beutler, Bruce A.
; APPLICANT: Bazoni, Flavia M.
; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY

TITLE OF INVENTION: SIGNAL
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/762.308
FILING DATE: 09-DEC-1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/224,593
FILING DATE: 05-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: USSD:335--1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 418-3000
TELEFAX: 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-762-308-10

Query Match 50.5% Score 690.4 DB 2 Length 1956;
Best Local Similarity 72.2% Pred No. 3.3e-156;
Matches 975; Conservative 0; Mismatches 351; Indels 24; Gaps 5;
1 ATGGGCTCTCTCCAGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
96 ATGGGCTCTCTCCAGCGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 155
61 GGAATATACCTCTCAAGGCTTATTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
156 GGAATATACCTCTCAAGGCTTATTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 215
121 GATAGTGTGTGCTCCAGGAAATATATATCCAGCTGCAAAATTAATTCGATTGCTGTACC 180
216 GATAGTGTGTGCTCCAGGAAATATATATCCAGCTGCAAAATTAATTCGATTGCTGTACC 275
181 AAGTGCACAAAGAAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
276 AAGTGCACAAAGAAAGAACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 335
241 TGCAGGAGTGTGAGAGGAGGCTCTTACAGGCTTCAAGAAACACCACTGACAGACAGTGCCTC 300
336 TGCAGGAGTGTGAGAAAGGAGGACCTTTACGCTTCCAGAAATTAATTCAGGAGAGTGTCTC 395
301 ACCTGCTCCAAATGCGGAAAGAAATGAGGCTCAGGTGAGATGCTCTTCTGACAGTGCAGC 360
396 ACCTGCTCCAAATGCGGAAAGAAATGAGGCTCAGGTGAGATGCTCTTCTGACAGTGCAGC 455
361 CGGAGACACCGTGTGCTGCTGAGAGAAACAGTACCGGCAATTAATGAGTGAAGAAACCTT 420
456 AAGGACACCGTGTGCTGCTGAGAGAAACAGTACCGGCAATTAATGAGTGAAGAAACCTT 515
421 TTCAGAGTGTAAATTTGACAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
516 TTCAGAGTGTGAGTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
481 AAACAGAACACCGGTGACAGCTGCACATGCAAGGTTTCTTTCTAAGAAAAAGAGTGTGC 540

